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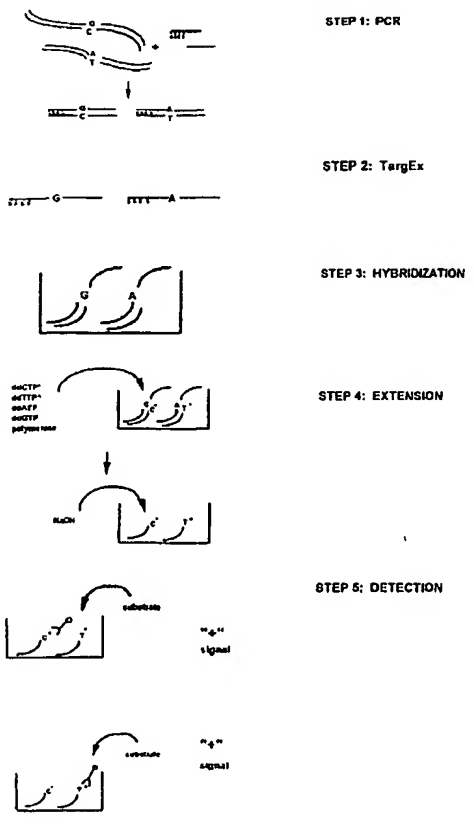


(57) Abstract: The present invention provides oligonucleotides that can be used to determine the presence, absence or identity of a single nucleotide polymorphism (SNP), kits containing such oligonucleotides, and methods of genotyping a nucleic acid sample using such oligonucleotides.

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# GENOTYPING REAGENTS, KITS AND METHODS OF USE THEREOF

## Background

Sequencing the human genome has provided information to dramatically change the way diseases are studied, diagnosed and treated. The fields of pharmacogenomics and pharmacogenetics focus on the variability and diversity of DNA, and how this diversity can impact biology, including response to drugs. The most common form of genetic diversity is thought to come in the form of individual DNA bases being different than the corresponding base in the average population. These single nucleotide polymorphisms ("SNPs") are a natural form of mutation, which are hereditary in nature. SNPs are viewed as both direct and indirect markers for many human diseases. Therefore, the analysis, or "scoring," of SNPs to determine their role in disease and drug efficacy can lead to the development of powerful diagnostics and therapeutics.

Adverse drug reactions (ADRs) represent the leading cause of hospitalization and mortality in the U.S., resulting in over 1.5 million hospitalizations and 100,000 deaths per year (J. Lazarou, et.al. in *The Journal of the American Medical Association (JAMA)*, (1998, 1200-1205). In addition, many promising drugs developed by pharmaceutical companies never make it through clinical development because of genetically based adverse reactions (ADRs) in a small number of patients. Therefore, scoring SNPs can identify at risk patients before the drug is prescribed and salvage potentially

useful new drugs. Alternatively, patients with SNP-induced variations in their conditions, evident in diseases like hypertension, can be identified and then prescribed the drug most appropriate for their genetic variant. Therefore, SNP analysis will be used to streamline drug discovery and development leading to safer and more effective tailor-made drugs.

Accordingly, new reagents are needed that can be used to identify whether heretofore unknown SNPs are present or absent from a given nucleic acid sample. The present invention satisfies this need and provides related advantages as well.

## Summary of the Invention

In accordance with the present invention, there are provided oligonucleotides that can be used to determine the presence, absence or identity of a single nucleotide polymorphism. Invention oligonucleotides include genotyping oligonucleotides that hybridize with a portion a nucleic acid sequence listed in column 4 of Table 1, or complementary sequence thereof, and amplification oligonucleotides.

In accordance with another embodiment of the invention, there are provided kits useful for determining the presence, absence or identity of a single nucleotide polymorphism. In one embodiment, an invention kit comprises an oligonucleotide that hybridizes with a portion of a nucleic acid sequence listed in column 4 of Table 1, or complementary sequence thereof. In another embodiment, an invention kit comprises amplification oligonucleotides of columns 1 and 2 of Table 1. Also provided is an invention kit comprising an

oligonucleotide that hybridizes with a portion of a nucleic acid sequence listed in column 4 of Table 1, or complementary sequence thereof and two amplification primers.

Another embodiment of the invention provides methods of genotyping a nucleic acid sample by hybridizing a genotyping oligonucleotide to a nucleic acid sequence listed in column 4 of Table 1, or complementary sequences thereof. The genotyping oligonucleotide can then be employed in a variety of reactions, such as, for example, a primer extension reaction. Also provided is a method of genotyping a nucleic acid sample by amplifying a target nucleic acid sequence and performing a single-nucleotide primer extension reaction employing a genotyping oligonucleotide that hybridizes to the target nucleic acid sequence.

## Brief Description Of The Figures

Figure 1 shows a schematic for genotyping a heterozygous nucleic acid sample containing two target nucleic acids using the particular primer extension reaction referred to as Single Nucleotide Primer Extension (SNPE) and/or GBA. In step 1, genomic DNA is amplified using a pair of PCR primers from columns 1 and 2 of the same row of Table 1 herein, in which the five most 5' nucleotides of one of the two PCR primers are linked by four exonuclease-resistant phosphorothioated linkages (e.g., 5' C-(p)-G-(p)-C-(p)-A-(p)-GTCTCAGGCCAGCT 3', for SEQ ID NO:2, where "-(p)-" represents a phosphorothioate linkage). The PCR primers are complementary to sequences flanking either side of a specific nucleotide site (e.g., the site of a SNP) in the genomic DNA, thus resulting in an amplified nucleic acid

(the target nucleic acid) containing this specific site. In step 2, the amplified PCR product target nucleic acid is subjected to T7 gene 6 exonuclease digestion, which removes the strand of the target nucleic acid that did not include the 5' phosphorothioated linkages, resulting in a single-stranded target nucleic acid. In step 3, the genotyping primer (or SNPE primer) is hybridized with the single stranded target nucleic acid such that the specific nucleotide of the target nucleic acid that is to be analyzed (i.e., the SNP) is not hybridized, and is immediately adjacent the 3' end of the genotyping primer. In step 4, a terminator reagent mixture comprising dideoxy terminators corresponding to A, C, G and T, together with a polymerase, are added to the target nucleic acid-genotyping primer complex. The polymerase extends the genotyping primer by a single base, consisting of one of the four terminators, where the added terminator base is complementary to the SNP to be determined. The terminator base that is added to the genotyping primer is labeled with a detectable marker. In the second part of step four, NaOH is added to dissociate the target nucleic acid strand which is washed away, while the genotyping primer, fixed to a solid support, remains. In step 5, a detection reagent is added, if necessary, to generate signal from the detectable marker. This can be performed in an ELISA format where an enzyme-linked antibody specific for the detectable marker of a terminator is contacted with the extended genotyping primer. When detectable markers that can be distinguished from each other are used, multiple alleles can be identified in a single well. For example, as illustrated in step 5, two alleles can be identified (C and T) by the sequential use of antibodies selective for each of the terminators (ddCTP and ddTTP).

Figures 2A and 2B show schematics for genotyping a homozygous nucleic acid sample using the Single Nucleotide Primer Extension (SNPE) by the enzyme-linked immunosorbant assay (ELISA) detection method after amplification using a phosphorothioated primer and exonuclease digestion. In figure 2A, the template strand indicated in the figure is a representative target nucleic acid molecule (such as those listed in SEQ ID NO:4n+4). The SNPE primer indicated in the figure is a representative genotyping primer (such as those listed in SEQ ID NO:4n+3). The nucleotide to be interrogated is indicated as the SNP to be typed. Primer extension is performed as described herein, in which the polymerase extension step can be performed in the presence of the terminators ddATP, ddGTP, fluorescein-ddCTP and biotin-ddUTP. The last two terminators are linked to detectable markers. Figure 2B shows the detection step after the single nucleotide primer extension results in the addition of fluorescein-ddCTP onto the 3'-end of the SNPE primer. The diagram illustrates the interaction of alkaline phosphatase-conjugated anti-fluorescein antibody and the generation of signal at $OD_{405}$ after the addition of PNPP (p-nitrophenyl phosphate) substrate. Since the biotin-ddUTP is not incorporated, the anti-biotin horse radish peroxidase (HRP)does not bind to the primer, no reaction with the TMB (tetramethylbenzidine) substrate occurs and, hence, no signal is generated at $OD_{620}$.

Figure 3 shows a scatterplot of $OD_{405}$ (X-axis) versus $OD_{620}$ (Y-axis) resulting from SNPE that demonstrates a result that is heterozygous. The PCR primers used were oligonucleotides of SEQ ID NOs:25 and 26. The SNPE primer used was an oligonucleotide with SEQ ID NO:27. The targeted nucleic acid with the suspected polymorphism contains the sequence of SEQ ID NO:28. SNPE

was performed using fluorescein-ddCTP and biotin-ddUTP. The Y-axis corresponds to signal obtained from ddUTP incorporation and the X-axis corresponds to signal obtained from ddCTP incorporation. Each circle (●)indicates a result with a specific test sample (unknown) from an individual genomic DNA. Plus (+) symbols are positive controls using a synthetic template. Crosses (x) are negative controls where no PCR is performed.

## Detailed Description of the Invention

In accordance with the present invention, there are provided oligonucleotides that can be used to determine (genotype) the presence, absence or identity of a single nucleotide polymorphism (SNP) at a preselected site in a human genomic nucleic acid sample. The location of the SNP in each SNP-containing oligonucleotide set forth in column 4 of Table 1 (also referred to herein as SEQ ID NO:4n+4, wherein n=0 through 934) herein corresponds to the nucleotide position on each SEQ ID NO:4n+4 that is immediately adjacent the nucleotide complementary to the 3' end of the corresponding genotyping oligonucleotide set forth in column 3 of the same row of Table 1. The nucleotide set forth on SEQ ID NO:4n+4 corresponding to the SNP site corresponds to the predominant polymorphism.

As set forth in Table 1, each row of oligonucleotides disclosed corresponds to a set of oligos useful for genotyping a nucleic acid sample for the presence or absence, or identity of a particular SNP. The oligonucleotides set forth in columns 1 and 2 of Table 1 (also referred to herein as SEQ ID NO:4n+1 and SEQ ID NO:4n+2, respectively, where n=0 through 934) are

used as primers to amplify the nucleic acid sample having the corresponding SNP-containing oligonucleotide from the same row in Table 1 (referred to as SEQ ID NO:4n+4, where n=0 through 934). See Figure 1. Once the nucleic acid sample having the corresponding SNP-containing oligonucleotide has been amplified, the corresponding genotyping oligonucleotide from column 3 (referred to as SEQ ID NO:4n+3, where n=0 through 934) of the same row in Table 1 is used to genotype the target nucleic acid, preferably by a primer extension reaction.

As used herein, the term "oligonucleotide", "oligo" or grammatical variations thereof, refers to polynucleic acid that can be either DNA or RNA. Invention oligos can be produced by methods well-known in art such as described in the Examples hereinafter; or the oligos can be purchased from commercial oligonucleotide production companies.

As used herein, the phrase "SEQ ID NO:4n+3, wherein n=0 through 934" refers to the group of oligonucleotides in the Sequence Listing that are set forth in column 3 of Table 1 herein (where n=(row number - 1). For example, n=0 corresponds to SEQ ID NO:3, n=1 corresponds to SEQ ID NO:7,..., n=934 corresponds to SEQ ID NO:3739 of the Sequence Listing. Likewise, SEQ ID NO:4n+1, SEQ ID NO:4n+2, and SEQ ID NO:4n+4, wherein n=0 through 934, refers to the groups of oligonucleotides set forth in columns 1, 2 and 4, respectively, of Table 1 herein.

The oligonucleotides set forth in column 3 of Table 1 (SEQ ID NO:4n+3, where n=0 through 934) are also referred to herein as genotyping oligonucleotides. In addition, for each SNP located in each oligonucleotide

set forth in column 4 of Table, there are at least four potential genotyping oligonucleotides (e.g., genotyping primers) that are hybridizable to the region one nucleotide removed from either 5' or 3' end of the SNP nucleotide (two for each strand). Two of the genotyping primers (one for each target nucleic acid strand) are complementary to the target nucleic acid and have their 3' ends one nucleotide 3' to the SNP nucleotide. These primers can be used, for example, in a polymerase primer extension reaction such as described in Goelet, P. et al., U.S. Pat No.5,888,819 and Nikiforov, T.T. et al., U.S. Pat. No. 5,518,900, which are herein incorporated by reference. The other two primers are complementary to the target nucleic acid and have their 5' ends one nucleotide 5' to the SNP nucleotide. These primers can be used in, for example, a ligase/polymerase genotyping reaction such as described in Nikiforov, T.T. et al., U.S. Pat. No. 5,679,524, or a nucleotide and terminator mixture reaction such as described in Soderlund et al., U.S. Pat. No. 6,013,431 or by Koster et al., U.S. Pat. No. 6,043,031, which is herein incorporated by reference.

In addition, the oligonucleotides set forth in column 3 of Table 1 (SEQ ID NO:4n+3, where n=0 through 934) can be made one nucleotide longer such that the nucleotide at the 3' end lies complementary to the SNP nucleotide. These primers can be used in alternate genotyping methods, for example, in allele-specific polymerase chain reaction (AS-PCR)(Newton et al., 1989, Nucl Acids Res 17:2503-2516), ligase chain reaction (LCR)(Barrany, 1991, PNAS, USA, 88: 189-193), or oligonucleotide ligation assay (OLA) (Landegren et al., 1988, Science 241:1077), where the 3' nucleotide of the genotyping primer determines the presence of the SNP nucleotide.

In addition, the oligonucleotides set forth in column 3 of Table 1 (SEQ ID NO:4n+3, where n=0 through 934) can be made one or more nucleotides shorter such that the genotyping primers are complementary to the target nucleic acid and have their 3' ends two or more nucleotides 3' to the SNP nucleotide. These primers can be used in, for example, a labeled nucleotide and terminator mixture reaction such as described in Soderlund et al., U.S. Pat. No. 6,013,431 or by Koster et al., U.S. Pat. No. 6,043,031, which is herein incorporated by reference.

The genotyping primer can be an oligodeoxyribonucleotide (DNA), an oligoribonucleotide (RNA), or a copolymer of deoxyribonucleotides and ribonucleotides. The genotyping primer can be either natural or synthetic. The genotyping primer can be synthesized either enzymatically in vivo, enzymatically in vitro, or non-enzymatically in vitro. The genotyping primer can include modifications of the ribose-phosphate backbone, such as phosphorothioate or methylphosphonate or other backbone modifications such as peptide nucleic acid (PNA). The genotyping primer can also include modifications of the nucleotide bases. The genotyping primer can be labeled with a detectable marker; this detectable marker can be different from any detectable marker present in the reaction mixture or any detectable marker attached to the target nucleic acid. In addition, for use with single-nucleotide primer extension reactions, the genotyping primer must be capable of hybridizing or annealing with nucleotides present in the target nucleic acid, immediately adjacent to, and upstream of, the nucleotide base to be identified. One way to accomplish the desired hybridization is to have the template-dependent primer be substantially

complementary or fully complementary to the known base sequence immediately adjacent to the base to be identified. The genotyping primer may be bound to a solid surface such as described in U.S. Pat. No. 5,610,287, incorporated herein by reference in its entirety. Multiple different genotyping primers can be immobilized on a surface to create an array, thus allowing the determination of multiple genotypes in a single reaction. Multiple different genotyping primers with distinct attachment means ("tags") can used for multiplex single nucleotide primer extension in solution and subsequently separated for discrete detection, such as on a nucleic acid array comprising nucleic acids complementary to the attachment means of the genotyping primers ("tag arrays").

Genotyping oligonucleotides of the invention can be as long as the nucleotide distance between an amplification primer and the SNP nucleotide, preferably not overlapping the amplification primer sequence, preferably less than 90 nucleotides, preferably less than 50 nucleotides, more preferably between 14 and 50 nucleotides, most preferably between 17 and 30 nucleotides.

When invention genotyping oligonucleotides are used in, for example, single-primer-extension reactions, hairpin loop structures can form due to self-complementarity of the nucleotides sequences of the oligo/primer. In order to disrupt the hairpin loop structure formation, "single-nucleotide-spacers" can be inserted in the midst of the hairpin loop structure. As used herein, the term "single-nucleotide-spacer" refers to any non-Watson-Crick moiety incorporated within an oligonucleotide for the purpose of weakening nucleic acid

duplex stability without altering the fidelity of the surrounding Watson-Crick base pairs. Thus, modifications to genotyping oligonucleotides contemplated herein are for the purpose of destabilizing duplex formation, specifically disfavoring intrastrand folding in favor of interstrand pairing. The location of single-nucleotide-spacers are set forth in the Sequence Listing and column 3 of Table 1 as an "X". Such moieties are well-known and available in the art and can include anucleosidic moieties, abasic moieties, non-naturally occurring nucleotide analogs, and non-Watson/Crick base moieties.

As used herein, the term "anucleosidic moieties" refers to moieties that approximate the spacing of the phosphoribose linkage. Thus, anucleosidic sites are contemplated herein as space-holders between neighboring phosphates along the oligo backbone. Examples of anucleosidic moieties for use in invention oligonucleotides include phosphoramidite-coupled multicarbon aliphatic chains that lack a nucleotide base and approximate the internucleotide spacing. For example, a C-3 linker used in DNA synthesis (3-(4,4'-Dimethoxytrityloxy)propel-1-phosphoramidite) (Glen Research, Sterling, VA) will have the approximate spacing of one nucleotide within a nucleic acid chain. Other anucleosidic sites include ethyl-like C2 and C1 linkers, rather than C3. C2- and C3-linkers are preferred as single-base length analogs. Larger anucleosidic spacers are contemplated herein having stretches of a few C2 or C3 linkers, or by incorporating a single C6 linker (for a two-base gap), or C9 (for 3 bases), and so forth up C18 linkers, and the like.

As used herein, the phrase "abasic moiety" refers to moieties that approximate the conformation of a

nucleotide but are chemically distinct from nucleotides, which include sugars or sugar analogs without base moieties. For example, an abasic site consists of the sugar-phosphate backbone without the base, such as tetrahydrofuran-phosphate (dSpacer; Glen Research, Sterling, VA), can be used as a nucleotide analog. Other backbones include those in which one or two of the non-bridging oxygen atoms of the phosphate moiety of a nucleotide have been replaced with a sulfur-containing group (especially a phosphorothioate), an alkyl group (especially a methyl or ethyl alkyl group), a nitrogen-containing group (especially an amine), and/or a selenium-containing group. In addition, peptide nucleic acids (PNAs)(Buchardt O, *Trends Biotechnol* 1993 Sep;11(9):384-6) or a carbohydrate are alternate backbones that can be used. It is contemplated that abasic modifications of these backbone types can be used as nucleotide analogs.

As used herein, "non-natural base variations" are non-canonical bases often referred to as "degenerate bases" since they exhibit some ability to base pair to any of the 4 standard bases. Exemplary non-natural base variations include, for example, "purine" and "pyrimidine" (which would be the structural scaffolds for A/G and C/T, respectively), as well as fluorine-derivatized bases, and the like. Examples of other non-natural base variations include 5-nitroindole, 3-nitropyrrole, and inosine. Numerous other "natural" base modifications that result from carcinogen exposure are also contemplated herein (see, e.g., Glen Research Catalog). The single nucleotide spacer can also include nucleotide ribose or deoxyribose analogs.

As used herein, the phrase "naturally occurring, non-Watson/Crick, bases" refers to any naturally occurring canonical base other than dA, dC, dG, dT. Common bases would be doexyinosine (dI) and deoxyuridine (dU). Other naturally occurring base variants can be found in tRNA sequences, and the like.

The single nucleotide spacer can also include non-complementary Watson/Crick nucleotide bases. An example of a mismatched nucleotide base would be the substitution of a thymidine base with an adenine base such that the intra helical base pair would be A:A instead of T:A and hence disrupt base pairing. For example, it is well known that some non-Watson/Crick pairs have moderate stability, such as G/T pairs. For any base pair, there are 6 potential mis-pairs using the standard 4 bases.

As used herein, the term "hybridize", or grammatical variations thereof, refers to the ability of two strands of nucleic acid molecules to hydrogen bond in a sequence dependent manner. For example, under appropriate conditions, complementary nucleotide sequences can hybridize to form double stranded DNA or RNA, or a double stranded hybrid of RNA and DNA. Nucleotide changes in the complementary sequence that disrupt base-pairing result in a decreased stability of the hybrid. These concepts are known in the art and described in Sambrook et al., Molecular Cloning: A Laboratory Manual 2nd ed. (1989), which is incorporated herein by reference.

Stringency levels used to hybridize a given probe with target-DNA can be readily varied by those of skill in the art. The phrase "stringent hybridization"

is used herein to refer to conditions under which nucleic acid hybrids are stable. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature ($T_m$) of the hybrids. In general, the stability of a hybrid is a function of GC content, cation concentration, formamide concentration and temperature. Typically, the hybridization reaction is performed under conditions of lower stringency, followed by washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions.

As used herein, the phrase "moderately stringent hybridization" refers to conditions that permit target-DNA to bind a complementary nucleic acid that has about 60% identity, preferably about 75% identity, more preferably about 85% identity to the target DNA; with greater than about 90% identity to target-DNA being especially preferred. Preferably, moderately stringent conditions are conditions equivalent to hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.2X SSPE, 0.2% SDS, at 65°C.

The phrase "high stringency hybridization" refers to conditions that permit hybridization of only those nucleic acid sequences that form stable hybrids in 0.018M NaCl at 65°C (i.e., if a hybrid is not stable in 0.018M NaCl at 65°C, it will not be stable under high stringency conditions, as contemplated herein). High stringency conditions can be provided, for example, by hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.1X SSPE, and 0.1% SDS at 65°C.

The phrase "low stringency hybridization" refers to conditions equivalent to hybridization in 10% formamide, 5X Denhart's solution, 6X SSPE, 0.2% SDS at 42°C, followed by washing in 1X SSPE, 0.2% SDS, at 50°C. Denhart's solution and SSPE (see, e.g., Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989) are well known to those of skill in the art as are other suitable hybridization buffers.

As used herein, the phrase "immediately adjacent the 3' end" refers to a specific first nucleotide position, typically on the target nucleic acid or on a nucleic acid having SEQ ID NO:4n+4, or complementary sequences thereof, which is immediately 5' of a second nucleotide position on the same nucleic acid, in which the second nucleotide position is complementary to the 3'-end nucleotide of SEQ ID NO:4n+3 or complementary sequence thereof. For example, Figure 2A shows a nucleotide sequence representative of a target nucleic acid sequence or a nucleic acid sequence having SEQ ID NO:4n+4, labeled "Template strand." Figure 2A also shows a nucleotide sequence representative of a nucleic acid sequence having SEQ ID NO:4n+3, labeled "SNPE primer." The 3'-end nucleotide of the SNPE primer is an "A" which is complementary to a "T" on the Template strand. The nucleic acid immediately 5' of the "T" on the Template strand is a "G," and is labeled in the figure "SNP to be typed. Accordingly, the "G" nucleotide on the Template strand, labeled as the SNP to be typed, is "immediately adjacent the 3' end" of the SNPE primer in Figure 2A.

Preferably, the invention oligonucleotides corresponding to SEQ ID NOs:4n+1 and 4n+2, where n=0

through 934 (i.e., columns 1 and 2 of Table 1) can be used as two amplification primers for increasing the amount of target nucleic acids (set forth in column 4 of Table 1) containing the SNP. In addition, in view of the target nucleic acids disclosed herein in column 4 of Table 1, those of skill in art can readily design additional amplification primers that can amplify larger target nucleic acid fragments comprising the target nucleic acids set forth in column 4. Likewise, it is contemplated herein that those of skill in art can readily design additional amplification primers that can amplify smaller target nucleic acid fragments, so long as the smaller target nucleic acid comprises the SNP-site set forth in column 4. The amplification primer pairs are designed such that the primers generate a target nucleic acid strand complementary to the genotyping primer and resistant to degradation, for example, by 5'-3' exonuclease.

As used herein, a nucleic acid that is "resistant to degradation" or "degradation-resistant" is a nucleic acid that is resistant to chemical degradation, acid hydrolysis, base hydrolysis, or other chemical-induced hydrolysis, or is resistant to enzymatic degradation. A nucleic acid that is resistant to enzymatic degradation can be resistant to exonuclease activity, endonuclease activity, and the like. In a preferred embodiment, a nucleic acid that is resistant to degradation is resistant to 5'-3' exonuclease activity, by using phosphorothioation, and the like.

A method of using 5'-3' exonuclease in the preparation of target nucleic acids is the subject of Nikiforov et al., U.S. Patent 5,518,900, which is herein incorporated by reference. Examples of 5'-3' exonuclease

resistant nucleic acids are disclosed in Zon, G. et al., (Anticancer Drug Design 6:539-568 (1991)) and Goodchild, J. et al. (Bioconjugate Chem. 1:613-629 (1990), both of which are incorporated herein by reference in their entirety. In general, suitable degradation-resistant nucleotide derivatives in which one or two of the non-bridging oxygen atoms of the phosphate moiety of a nucleotide have been replaced with a sulfur-containing group (especially a phosphorothioate), an alkyl group (especially a methyl or ethyl alkyl group), a nitrogen-containing group (especially an amine), and/or a selenium-containing group, etc. Other modifications that confer degradation resistance such as 5'-3' exonuclease resistance can be used, for example, peptide nucleic acids (PNAs) (Buchardt, O. *supra*) or 2'-O-methyl ribose modified nucleic acids Srivastava S., C. et al., U.S. Pat. No. 5,214,135. Degradation resistance is preferably achieved by the primer containing a phosphorothioate modification at the 5' end of the nucleic acid and, in a preferred embodiment, containing four phosphorothioate linkages at the 5' end.

The selected nucleotide derivative is suitable for *in vitro* primer-mediated extension and provides nuclease resistance to the region of the nucleic acid molecule in which it is incorporated. In a preferred embodiment, a nucleotide derivative confers resistance to exonucleases that attack double-stranded nucleic acids from the 5'-end (5'-3' exonucleases). Examples of such exonucleases include bacteriophage T7 gene 6 exonuclease and bacteriophage lambda exonuclease. Both exonucleases are inhibited by the presence of phosphorothioate bonds so as to allow the selected degradation of the unmodified nucleic acid strand. However, any double-strand specific, 5'-3' exonuclease can be used for this process,

provided its activity is affected by the presence of the modified nucleotides. The preferred enzyme when using phosphorothioate derivatives is the T7 gene 6 exonuclease, which shows maximal enzymatic activity in the same buffer used for many DNA dependent polymerase buffers including Taq polymerase. The 5'-3' exonuclease resistant properties of phosphorothioate derivative-containing DNA molecules are discussed, for example, in Kunkel, T.A. et al. (In: Nucleic Acids and Molecular Biology, Vol. 2, 124-135 (Eckstein F. et al., eds.), Springer-Verlag, Berlin, (1988)). The 3'-5' exonuclease resistant properties of phosphorothioate nucleotide containing nucleic acid molecules are disclosed in Putney et al. (Proc. Natl. Acad. Sci. (U.S.A.) 78:7350-7354 (1981)) and Gupta A.P. et al. (Nucl. Acids Res., 12:5897-5911 (1984)).

The amplification primers can be used to generate amplified nucleic acid products by any *in vitro* amplification method known to those skilled in the art that uses a DNA dependent or RNA dependent DNA or RNA polymerase. The preferred method is the polymerase chain reaction (PCR) that involves template-dependent extension using thermally stable DNA polymerase (Mullis K et al, Cold Spring Harbor Symp. Quant. Biol. 51:263-273 (1986); Erlich H et al.,EP 50,424; EP 84,796, EP 258,017, EP 237-362; Mullis K., EP 201,184; Mullis, K. et al, U.S. Pat. No. 4,683,202; Erlich, H., U.S. Pat. No. 4,582,788; and Saiki, R. et al., U.S. Pat. No. 4,683,194), incorporated herein by reference. PCR achieves the amplification of a specific nucleic acid sequence using two oligonucleotide primers complementary to regions of the sequence to be amplified. Extension products incorporating primers then become templates for subsequent amplification steps. Reviews of the polymerase chain reaction are provided by

Mullis, K.B., (*supra*); Saiki, R.K. et al., (Bio/Technology 3:1008-1012 (1985)); and Mullis, K.B. et al. (Meth. Enzymol. 155:335-350 (1987)), which is incorporated herein by reference.

Other nucleic acid amplification procedures can be used and include transcription-based amplification systems (Kwoh, D. et al., Proc. Natl. Acad. Sci. (U.S.A.) 86:1173 (1989)); Gingeras T.R. et al., PCT appl. WO 88/10315 (priority: U.S. patent application Ser. Nos. 064,141 and 202,978); Miller, H.I. et al., PCT appl. WO 89/06700 (priority: U.S. patent application Ser. No. 146,462); Davey, C. et al., (European Patent Application Publication No. 329,822)), RNA-dependent RNA amplification (Qβ replicase (Kramer, F.R. et al., U.S. Pat. No. 4,786,600), and ligation-based amplification systems (Wu, D.Y. et al., Genomics 4:560 (1989)).

Amplification primers can be any length but are preferably as long as 90 nucleotides, preferably between 14 to 50 nucleotides, more preferably between 17 and 30 nucleotides.

In accordance with another embodiment of the invention, methods are provided for genotyping a nucleic acid sample comprising hybridizing an invention oligonucleotide to the nucleic acid sample, and preferably, performing a primer extension reaction .

As used herein, the term "genotyping" refers to determining the presence, absence or identity of a nucleotide base (e.g., a SNP) at a specific position in a target nucleic acid. First, a sample containing the target nucleic acid is treated, if such nucleic acid is double-stranded, so as to obtain unpaired nucleotide

bases spanning the specific position. If the target nucleic acid is single-stranded, this step is not necessary. Second, the sample containing the target nucleic acid is contacted with a genotyping oligonucleotide (also referred to as a genotyping primer) under hybridizing conditions. The genotyping oligonucleotide is capable of hybridizing with a stretch of nucleotide bases present in the target nucleic acid, adjacent the nucleotide base to be identified (e.g., a SNP), so as to form a duplex between the genotyping oligo and the target nucleic acid. When the genotyping oligonucleotide is "immediately adjacent" the nucleotide base to be identified (e.g., a SNP), the genotyping oligonucleotide hybridizes with the target nucleic acid in such a way that either the 3' or 5' end of the genotyping oligonucleotide is complementary to a nucleotide on the target nucleic acid that is located immediately 5' or 3', respectively, of the nucleotide base to be identified (see, e.g., Figure 2A and 2B). It is also contemplated herein that the invention genotyping oligos can be fragments of the oligos in column 3 of the Table 1 (i.e., SEQ ID NO:4n+3, n=0-934) hybridizable to the target nucleic acid and adjacent to the nucleotide base to be identified such that the 3' end of the genotyping oligo is 1 up to 10, preferably 3 up to 6, nucleotides upstream from the nucleotide base to be identified in the target nucleic acid.

As used herein , the phrase "primer extension" refers to enzymatic extension of the genotyping primer in the resultant duplex by one or more nucleotides, catalyzed, for example, by a DNA polymerase, and the like. Such primer extension thus depends on correct base pairing of the added nucleotide to the nucleotide base to be identified.

In one embodiment, the duplex of genotyping primer and target nucleic acid can then be contacted with a reagent containing at least two, but preferably four terminators, at least one of which terminators being labeled. The duplex of genotyping primer and the target nucleic acid is contacted with the reagent under conditions permitting base pairing of a complementary terminator present in the reagent with the nucleotide base to be identified and the occurrence of a template-dependent, primer extension reaction so as to incorporate a terminator at the 3' end of the primer. The net result is that the genotyping primer has been extended by one terminator. Next, the presence or absence of a labeled terminator at the 3' end of the extended genotyping primer is detected. The identity of the labeled terminator indicates which terminator has base paired to the next base in the target nucleic acid. Since the terminator is complementary to the next base in the target nucleic acid, the identity of the next base in the target nucleic acid is thereby determined.

It is also contemplated that the genotyping primer can be extended by a nucleic acid template-dependent ligation reaction. In such a reaction, a ligating oligonucleotide is used that hybridizes to the target nucleic acid only if the nucleotide residue corresponding to the SNP on the target molecule is complementary to the corresponding nucleotide on the ligating oligonucleotide. If such a ligating oligonucleotide hybridizes with the target nucleic acid, the ligating oligonucleotide and the genotyping oligonucleotide will be immediately adjacent each other. The genotyping primer and ligating primer can then be ligated by contacting the target nucleic acid, genotyping

primer and ligating oligonucleotide with a nucleic acid ligase. The ligation reaction can ligate the 5' end of the genotyping primer to the 3' end of the ligating primer, or alternatively, the ligation reaction can ligate the 3' end of the genotyping primer to the 5' end of the ligating primer. Either the genotyping primer or the ligating oligonucleotide can be labeled with a detectable marker. The detection of a ligation product indicates the presence of the SNP nucleotide targeted by the ligation primer.

As used herein, a detectable marker is any molecule or structure that can be detected by spectroscopic, scattering, emission, absorption, binding, or other known detection methods known in the art. Exemplary detectable markers include a radionuclide, a fluorochrome, a colorimetric agent, a magnetic substance, an electron-rich material such as a metal, a luminescent tag, or a detectable binding agent such as biotin. Preferably, the detectable marker is a fluorochrome or a detectable binding agent. More preferably, the detectable marker is a fluorescent dye or a detectable binding agent that can be bound by an antibody. In one embodiment, the detectable marker is biotin or fluorescein. A detectable binding agent refers to any substance that can bind a solid support, a probe molecule, or other molecule that binds the detectable binding agent and, in turn, is then detected or permits identification of the nucleic acid which is labeled with the detectable binding agent. For example, a detectable marker can be biotin which is bound by an antibody specific to biotin, whereupon the antibody can then be detected in an ELISA-based assay. Other detectable markers known in the art may be used in the invention assay, for example, markers listed in the catalog of

Molecular Probes (Eugene, OR), markers listed in the catalog of Synthegen (Houston, TX), and markers listed in WO 98/59066, which are all herein incorporated by reference.

It is further contemplated herein that one or more primer extension reactions, used in genotyping a nucleic acid sample comprising one or more different target nucleic acids, can be carried out in the same reaction vessel. In one embodiment, at least one terminator is labeled with a detectable marker. In another embodiment, one or more genotyping primers are each labeled with a detectable marker. Detection of identity of the SNPs on the one or more target nucleic acids can then be carried out using one of a variety of methods including spectroscopic detection of one or more detectable markers, separation of one or more nucleic acid sequences used to identify the identity of the corresponding one or more SNPs. Such methods for the detection of one or more SNPs in a single reaction vessel are described in WO 98/59066, which is herein incorporated by reference.

In a preferred embodiment, the primer extension reaction is a "single-nucleotide primer extension" as described, for example in United States Patent No. 5,679,524 and in United States Patent No. 5,888,819, incorporated herein by reference in their entirety. In this method, a genotyping primer hybridizes with the target nucleic acid immediately adjacent the nucleotide base to be identified, so as to form a duplex between the genotyping primer and the target nucleic acid such that the nucleotide base to be identified is the first unpaired base in the template target nucleic acid immediately downstream of the 3' end of the genotyping

primer in the duplex of genotyping primer and target nucleic acid. In this embodiment, primer extension will add a single terminator residue which is complementary to the base to be determined in the target nucleic acid. Identification of the terminator will thus provide identification of the base on the target nucleic acid to be determined.

Typically, two or more terminators are labeled, each labeled with a different detectable marker, thereby permitting simultaneous detection (and hence, identification) of the two or more labeled terminators. Preferably four terminators are labeled, each with a different detectable marker, thereby permitting simultaneous detection and identification of up to four labeled terminators.

In the embodiment in which only one terminator is labeled (a first labeled terminator), the above-described primer extension procedure can be repeated at least once, using a second labeled terminator that is different from the first labeled terminator. This process can be repeated once, twice or three times, using a different, labeled terminator for each repetition.

As used herein, the phrase "nucleic acid sample" refers to one or more of target nucleic acids, which can be from any source. The sample of target nucleic acids can be natural or synthetic (i.e., synthesized enzymatically in vitro). The sample of target nucleic acids can comprise deoxyribonucleic acids (DNAs), ribonucleic acids (RNAs), or copolymers of deoxyribonucleic acid and ribonucleic acid. The target nucleic acid can be a deoxyribonucleic acid (DNA), a ribonucleic acid (RNA), or a copolymer of

deoxyribonucleic acid and ribonucleic acid. The target nucleic acid can be synthesized enzymatically in vivo, synthesized enzymatically in vitro, or synthesized non-enzymatically. The sample containing the target nucleic acid or acids can comprise genomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof. The sample containing the target nucleic acid or acids can also comprise extragenomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof. Preferably, the target nucleic acid or acids are synthesized by amplification methods described herein. More preferably, the target nucleic acid or acids are synthesized by the polymerase chain reaction.

The sample can be taken from any organism, but is preferably human. Some examples of organisms to which the method of the subject invention is applicable include plants, microorganisms, viruses, birds, vertebrates, invertebrates, mammals, humans, horses, dogs, cows, cats, pigs, or sheep. For assay of genomic DNA, virtually any biological tissue samples can be used, including whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified by PCR, and the like, before analysis.

The target nucleic acid can comprise one or more moieties that permit affinity separation of the target nucleic acid from the unincorporated reagent and/or the primer. The target nucleic acid can comprise biotin which permits affinity separation of the target nucleic acid from the unincorporated reagent and/or the primer via binding of the biotin to streptavidin which is attached to a solid support. The sequence of the target nucleic acid can comprise a DNA sequence that permits

affinity separation of the target nucleic acid from the unincorporated reagent and/or the primer via base pairing to a complementary sequence present in a nucleic acid attached to a solid support. The target nucleic acid can be labeled with a detectable marker; this detectable marker can be different from any detectable marker present in the reagent or attached to the primer.

In a preferred embodiment, the target nucleic acid sequence is synthesized by an amplification method and is modified at the 5' end to prevent hydrolysis by, for example, exonuclease activity, as described herein. See, for example, United States Patent 5,518,900, which describes a method for generating single-stranded nucleic acid molecules containing nuclease-resistant nucleotides.

The genotyping primer can comprise one or more moieties that permit affinity separation of the primer from the unincorporated reagent and/or the target nucleic acid. The genotyping primer can comprise biotin which permits affinity separation of the primer from the unincorporated reagent and/or target nucleic acid via binding of the biotin to streptavidin which is attached to a solid support. The sequence of the genotyping primer can comprise a DNA sequence that permits affinity separation of the primer from the unincorporated reagent and/or the target nucleic acid via base pairing to a complementary sequence present in a nucleic acid attached to a solid support.

In another embodiment of the invention, a method is provided for genotyping a nucleic acid sample comprising:

a) amplifying a target nucleic acid sequence that hybridizes to an oligonucleotide selected from the group of SEQ ID NOs consisting of 4n+3, or complementary sequences thereof; and

b) performing a single-nucleotide primer extension reaction employing an oligonucleotide comprising a nucleic acid selected from the group of SEQ ID NOs consisting of 4n+3, or complementary sequences thereof,

wherein n=0 through 934 and is the same value in both steps a and b.

As used herein, a target nucleic acid sequence that hybridizes to an oligonucleotide selected from the group of SEQ ID NOs consisting of 4n+3 or complementary sequences thereof refers to a target nucleic acid comprising a sequence substantially similar to at least a portion of nucleic acid of SEQ ID NO:4n+4, or complementary sequences thereof that hybridizes to a nucleic acid of SEQ ID NO:4n+3. Typically, such a target nucleic acid sequence will comprise the nucleic acid of SEQ ID NO:4n+4 with the exception of the nucleotide immediately adjacent the 3' end of the nucleic acid of SEQ ID NO:4n+3, which may or may not be present, where n is the same value for both SEQ ID NOs:4n+3 and 4n+4.

In a further embodiment of the invention, a kit is provided which contains at least one genotyping primer. As used herein, a kit refers to a genotyping system in kit form, comprising at least one invention genotyping primer, and optionally further comprising chain termination reagent in combination with a DNA polymerase with or without an associated 3' to 5'

exonuclease function, and an appropriate salt and cofactor mixture, in a suitable packaging material. Invention kits are useful for assaying for the presence or absence of a nucleotide at a specified location on one or more target nucleic acids. Preferably, the invention kit is useful for determining the identity of a nucleotide at a specified location on one or more target nucleic acids. To facilitate the assaying for the presence or absence, or determining the identity of the SNP nucleotide on the target nucleic acid, the invention kit provides a genotyping primer, one or more terminators, or both a genotyping primer and one or more terminators, that are labeled with a detectable marker.

The conditions for the occurrence of the template-dependent, primer extension reaction can be created, in part, by the presence of a suitable template-dependent enzyme. Some of the suitable template-dependent enzymes are DNA polymerases. The DNA polymerase can be of several types. The DNA polymerase must, however, be primer and template dependent. For example, E. coli DNA polymerase I or the "Klenow fragment" thereof, T4 DNA polymerase, T7 DNA polymerase ("Sequenase"), Thermus aquaticus DNA polymerase, or a retroviral reverse transcriptase can be used. RNA polymerases such as T3 or T7 RNA polymerase can also be used in some protocols. Depending upon the polymerase, different solution conditions and different temperature ranges are used for the hybridization and extension reactions.

The reagents of the subject invention typically permit the typing of nucleic acids of interest by facilitating the analysis of the 3' terminal addition of terminators to a specific primer or primers under specific hybridization and primer extension conditions.

Using only one terminator in the chain termination reagent as the nucleoside triphosphate substrate ensures addition of only one nucleotide residue to the 3' terminus of the primer in the polymerase reaction. Using all four terminators simultaneously ensures fidelity, i.e., suppression of misreading.

A genotyping primer of an invention kit comprises a genotyping primer as described above, which is capable of hybridizing to a target nucleic acid. An invention kit comprises one or more genotyping primers. In one embodiment of an invention kit, the genotyping primer(s) comprises any of SEQ ID NO:4n+3, or the complement thereof, where n=0 to 934. In another embodiment the genotyping primer(s) comprises a portion of any of SEQ ID NO:4n+4, or the complement thereof, where n=0 to 934. In yet another embodiment the genotyping primer(s) hybridizes with any of SEQ ID NO:4n+4, or the complement thereof, where n=0 to 934.

A suitable kit includes at least one invention genotyping primer, and optionally further comprising chain termination reagent in combination with a DNA polymerase with or without an associated 3' to 5' exonuclease function, and an appropriate salt and cofactor mixture, as a separately packaged chemical reagent(s) in an amount sufficient for at least one assay. Instructions for use of the packaged reagent are also typically included. Those of skill in the art can readily incorporate invention genotyping primers into kit form in combination with appropriate buffers and solutions for the practice of the invention methods as described herein.

In another embodiment, an invention kit comprises a genotyping primer and two amplification primers. This kit can also comprise chain termination reagent in combination with a DNA polymerase with or without an associated 3' to 5' exonuclease function, and an appropriate salt and cofactor mixture to be used in conjunction with the genotyping primer, and can also comprise nucleotide reagent in combination with a DNA polymerase with or without an associated 3' to 5' exonuclease function, and an appropriate salt and cofactor mixture to be used in conjunction with the amplification primers, in a suitable packaging material. Such invention kits are useful for (1) amplifying one or more target nucleic acid sequences in a nucleic acid sample and (2) assaying for the presence or absence of a nucleotide at a specified location on one or more target nucleic acids. Preferably, invention kits are useful for (1) amplifying one or more target nucleic acid sequences in a nucleic acid sample and (2) determining the identity of a nucleotide at a specified location on one or more target nucleic acids.

Preferably, a kit comprising one genotyping primer and two amplification primers comprises a genotyping primer that hybridizes to the sequence SEQ ID NO:4n+4 and amplification primers of the sequence SEQ ID NOs:4n+1 and 4n+2, where n=0 through 934 and the three oligonucleotides correspond to SEQ ID NOs having the same value for n.

More preferably, a kit comprising one genotyping primer and two amplification primers comprises a genotyping primer of the sequence SEQ ID NO:4n+3 and amplification primers of the sequence SEQ ID NOs:4n+1 and 4n+2, where n=0 through 934 and the three

oligonucleotides correspond to three consecutive SEQ ID NOs having the same value for n.

In yet another embodiment of the invention, a kit comprises two amplification primers. This kit can also comprise nucleotide reagent in combination with a DNA polymerase with or without an associated 3' to 5' exonuclease function, and an appropriate salt and cofactor mixture to be used in conjunction with the amplification primers, in a suitable packaging material. Such invention kits are useful for amplifying one or more target nucleic acid sequences in a nucleic acid sample.

A termination reagent of an invention kit refers to a reagent comprising at least one terminator. Preferably, a termination reagent comprises two terminators. More preferably, a termination reagent comprises three terminators. Most preferably, a termination reagent comprises four terminators. A termination reagent will comprise one or more terminators labeled with a detectable marker. Preferably, a termination reagent comprises two or more terminators labeled with a detectable marker. More preferably, a termination reagent comprises three or more terminators labeled with a detectable marker. Most preferably, a termination reagent comprises four or more terminators labeled with a detectable marker.

A nucleotide reagent of an invention kit for use in an amplification reaction refers to a reagent comprising at least one nucleotide triphosphate. Preferably, a nucleotide reagent comprises two nucleotide triphosphates. More preferably, a nucleotide reagent comprises three nucleotide triphosphates. Most

preferably, a nucleotide reagent comprises four nucleotide triphosphates.

In a particularly preferred embodiment, an invention kit comprises a collection reagents termed "Master Mix" as described in Example I. Exemplary Master Mix 2x is as follows: 768 mL of sterile, distilled water 200 mL of 10xPCR salts (100 mM Tris-HCl, pH 8.5, 500 mM KCl, 15 mM $MgCl_2$ and 0.01% Gelatin) and 8 mL of each dNTP stock (100 mM stocks of deoxyribonucleotide triphosphates dATP, dCTP, dGTP, and dTTP) in sterile, distilled $H_2O$. The final composition being: 50 mM Tris-HCl, pH 8.5, 100 mM KCl, 3 mM $MgCl_2$, 0.002% Gelatin, and 800 µM each dNTP. This solution can be stored at -20°C until use. Master mix can be prepared in a variety of different concentrations, described as a function of x, as the above example depicts 2x Master Mix. The concentration of the master mix employed herein may vary from 0.5x, 1x, 2x, or 5x, to as high as 10x, 20x, or 50x. Preferably, the master mix is from 2x to 5x.

In addition, in place of Tris-HCl, any other buffer which does not interfere with the enzymatic and/or detection processes of required to detect the presence, absence or identity of a SNP may be used. Such buffers include the so-called "Good buffers", and other organo-amino based buffers, and the like. Similarly, the pH may be adjusted to any range capable of carrying out the desired processes. The pH may range from as low as about 6.0, 7.0, or 8.0, to as high as about 8.5, 8.7, or 9.0. Preferably, the pH ranges from about 7.0 to about 8.7. More preferably, the pH ranges from about 8.0 to about 8.5. Buffer concentration may vary from as low as 10 mM, 25 mM or 50 mM, to as high as 75 mM, 100 mM or 200 mM.

Preferably, the buffer concentration is from 25 mM to 100 mM.

In place of KCl, other monovalent-cation salts can be used. Other exemplary monovalent-cation salts include salts with the cation: $NH_4^+$, alkalai metal ions $Li^+$, $Na^+$, $Rb^+$, $Cs^+$, and other monovalent cations. The anion can be any anion which does not adversely influence the amplification reaction. Exemplary anions are halide anions, $F^-$, $Cl^-$, $Br^-$, $I^-$, and other anions such as phosphate, sulfate, nitrate, and the like. The concentration of the monovalent salt can be as low as 15 mM, 40 mM, or 75 mM, to as high as 100 mM, 150 mM or 250 mM. Preferably, the monovalent-cation salt concentration is from about 75 to 150 mM.

In place of $MgCl_2$, other divalent-cation salts can be used. Other exemplary divalent-cation salts include salts with the cation: $Mg^{2+}$, $Ca^{2+}$, $Mn^{2+}$, $Cu^{2+}$, $Zn^{2+}$, $Cd^{2+}$, and other divalent cations. The anion can be any anion which does not adversely influence the amplification reaction. Exemplary anions are halide anions, $F^-$, $Cl^-$, $Br^-$, $I^-$, and other anions such as phosphate, sulfate, nitrate, and the like. The concentration of the divalent salt can be as low as 0.5 mM, 1 mM, or 3 mM, to as high as 5 mM, 10 mM or 25 mM. Preferably, the divalent-cation salt concentration is from about 1 mM to 10 mM.

In place of gelatin, other volume exclusion agents can be used such as polyvinyl pyrrolidone, polyethlene glycol, polyacrylamide, linear polyacrylamide, and the like. The volume exclusion reagent can be absent, or can be as low as 0.0001%, 0.0005% or 0.001%, to as high as 0.002%, 0.005% or 0.02%.

Preferably, the volume exclusion agent is about 0.001% to 0.005%.

The concentration of each of dCTP, dGTP, dATP and dTTP (i.e., the dNTPs) can vary in concentration from 250 μM, 500 μM, or 800 μM, to 1 mM, 1.5 mM or 2.5 mM. Preferably, the concentration of the dNTPs is about 500 μM to 1 mM.

As employed herein, the phrase "packaging material" refers to one or more physical structures used to house the contents of the kit, such as invention primers, and the like. The packaging material is constructed by well known methods, preferably to provide a sterile, contaminant-free environment. The packaging material has a label which indicates that the invention probes can be used for determining the presence or absence of, or preferably the identity of, a particular nucleotide on a target nucleic acid, thereby genotyping the target nucleic acid. In addition, the packaging material contains instructions indicating how the materials within the kit are employed to determine the presence or absence of, or preferably the identity of, a particular nucleotide on a target nucleic acid.

The packaging materials employed herein in relation to diagnostic systems are those customarily utilized in nucleic acid-based assay systems. As used herein, the term "package" refers to a solid matrix or material such as glass, plastic, paper, foil, and the like, capable of holding within fixed limits an isolated nucleic acid, oligonucleotide, or primer of the present invention. Thus, for example, a package can be a glass vial used to contain milligram quantities of a contemplated nucleic acid, oligonucleotide or primer, or

it can be a microtiter plate well to which microgram quantities of a contemplated nucleic acid probe have been operatively affixed.

"Instructions for use" typically include a tangible expression describing the reagent concentration or at least one assay method parameter, such as the relative amounts of reagent and sample to be admixed, maintenance time periods for reagent/sample admixtures, temperature, buffer conditions, and the like.

It is contemplated herein that each of the genotyping and amplification primers described herein can be used in the invention methods of genotyping nucleic acid samples, for example, to assess by association analysis the genotype of an individual, or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more single nucleotide polymorphisms. Phenotypic traits suitable for association analysis include diseases that have known but yet unmapped genetic components, e. g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria, and the like.

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, system, diseases of the nervous system and infection by pathogenic

microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulindependent and non-independent), systemic lupus erythematosus and Graves disease, and the like. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus, and the like.

Phenotypic traits also include characteristics such as longevity, appearance (e. g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Such correlations can be exploited in several ways. In the case of a strong correlation between a polymorphic form and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e. g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the

patient may have increased susceptibility by virtue of variant alleles. After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

In addition, determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally, National Research Council, The Evaluation of Forensic DNA Evidence (Eds. Pollard et al., National Academy Press, DC, 1996). Thus, each of the genotyping and amplification primers described herein can be used in the invention methods of genotyping nucleic acid samples, for example, to identify a distinguishing or unique set of forensic markers in an individual useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e. g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance (see, e.g, WO 95/12607). If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e. g.,

one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

In addition, each of the genotyping and amplification primers described herein can be used in the invention methods of genotyping nucleic acid samples, for example, to identify a distinguishing or unique set of markers in an individual useful for paternity analysis. The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child. If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match (see, e.g., WO 95/12607). If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The single nucleotide polymorphisms set forth in column 4 of Table 1 (also referred to herein as SEQ ID NO:4n+4, wherein n=0 through 934) may contribute to the phenotype of an organism in different ways. Some of these polymorphisms may occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Others of these polymorphisms may occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some of these polymorphisms may predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but yet unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits

also include characteristics such as longevity, appearance (e. g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a single or a set of polymorphisms (i. e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a chi-squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. Such correlations can be exploited in several ways as set forth above.

For example, in the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Thus, the methods of genotyping nucleic acid samples described herein can be used, for example, to diagnose any of more than 3000 genetic diseases currently known or to be identified,

e.g., hemophilias, thalassemias, Duchene Muscular Dystrophy (DMD), Huntington's Disease (HD), Alzheimer's Disease and Cystic Fibrosis (CF), and the like.

It is also contemplated herein that each of the genotyping and amplification primers described herein can be used in the invention methods of genotyping nucleic acid samples, for example, for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmocogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

All U.S. patents and all publications mentioned herein are incorporated in their entirety by reference thereto. The invention will now be described in greater detail by reference to the following non-limiting examples.

## Examples

### Example I

### Preparation of 2x Master Mix for PCR

A component of genotyping using SNPE is accurate and efficient amplification of the nucleic acid region being tested for the SNP. To facilitate control of the PCR used, a reaction mixture, referred to herein as "2x Master Mix," has been produced to achieve more successful PCRs.

2x Master Mix was prepared as follows: 10xPCR salts was 100 mM Tris-HCl, pH 8.5, 500 mM KCl, 15 mM $MgCl_2$ and 0.01% Gelatin, stored in a -20°C freezer. 100 mM stocks of deoxyribonucleotide triphosphates dATP, dCTP, dGTP, and dTTP (dNTPs) (LTI, Bethesda, MD) were made in sterile, distilled $H_2O$. To 768 mL of sterile, distilled water 200 mL of 10xPCR salts and 8 mL of each dNTP stock was added. The final composition was: 50 mM Tris-HCl, pH 8.5, 100 mM KCl, 3 mM $MgCl_2$, 0.002% Gelatin, and 800 µM each dNTP. The solution was stored at -20°C until use.

### Example II

### Single Nucleotide Polymorphism Detection by Single Nucleotide Primer Extension (SNPE)

Single nucleotide polymorphisms are the most common form of genetic diversity and are thought to be direct and indirect markers of many human diseases. The following example shows the use of Single Nucleotide

Primer Extension (SNPE) to identify the presence of SNPs. The method of SNPE is the subject of US Patent 5,888,819 and more recently described in detail by Reynolds et al. in *DNA Markers: Protocols, Applications, and Overviews* (ed. G. Caetano-Anolles), pp. 199-211, Wiley-Liss, New York, NY (1997), both of which are herein incorporated by reference.

The amplification primers listed herein (Table 1, columns 1 and 2) were selected to amplify the corresponding SNP-containing oligo in column 4, forming a PCR amplified target nucleic acid such that the primers do not overlap the corresponding genotyping (SNPE) primer in column 3.

SNPE primers were designed to be complementary to the phosphorothioate-modified strand of the PCR product target nucleic acid and ending one nucleotide base short 3' to the polymorphic site to be interrogated as described (Reynolds et al., *supra*). Either DNA strand can be a target for the SNPE primer as long as the phosphorothioate-modified strand of the PCR product is the complementary strand.

All oligonucleotides were synthesized by standard phosphoramidite chemistry on a PE Biosystems 392/394 DNA Synthesizer using Glen Research (Sterling, VA) reagents. Tetraethylthiuram sulfide (TETD; PE Biosystems, Foster City, CA) was used for phosphorothioate modification as per manufacturer's instructions. All oligonucleotides were deprotected in concentrated ammonia and desalted using NAP5 or NAP25 gel filtration columns (Amersham Pharmacia Biotech, Piscataway, NJ) as per manufacturer's instructions.

Genomic DNA from genetically diverse human individuals purchased from the Coriell Institute for Medical Research (Camden, NJ) was the source of DNA for PCR amplifications. The DNA sample was diluted with sterile, distilled $H_2O$ to a final concentration of 5 ng/µL before use.

PCR amplification of 10 ng of template genomic DNA was performed in 384-well plates under the following conditions: 10 mM Tris-HCl, pH 8.5, 50 mM KCl, 1.5 mM $MgCl_2$, 0.001% gelatin, 400 µM each of dATP, dCTP, dGTP, and dTTP, (from the 2x Master Mix) and 0.050 U/µL Platinum Taq (*Thermus aquaticus*) DNA polymerase, (LTI, Bethesda, MD) using 0.5 µM each primer concentration in a total volume of 5 µL. The PCR amplification was performed in a PTC-225 DNA Engine Tetrad thermocycler (MJ Research, Watertown, MA) using the following protocol: following a 2 minute denaturation step at 95°C thirty-five cycles were carried out, each consisting of denaturation (30 seconds at 94°C), annealing (2 minutes at 55°C), and extension (30 seconds at 72°C) steps. This was followed by a final extension step (1 min at 72°C) and hold (4°C).

Single stranded target nucleic acid DNA was prepared from the double-stranded PCR product by treatment with a 5'-3' DNA exonuclease. Briefly, 5 µL T7 gene 6 exonuclease (United States Biologicals, Swampscott, MA) in 0.5 M Tris-HCl, pH 7.5, 1 mM Dithiothreitol (DTT), and 0.01% acetylated Bovine Serum Albumin (BSA) was added to a final concentration of 0.45 U/µL and incubated for one hour at room temperature. The reaction was terminated by the addition of 5 µL of 3 x SNPE Salt (4.5M NaCl, 30 mM EDTA, and 3 mM cetyltrimethylammonium bromide (CTAB)). The DNA created

by PCR originating from the phosphorothioated primer is protected from nuclease digestion whereas the opposite strand with the unmodified primer is digested and hence will not interfere with the hybridizing strand to the immobilized genotyping (SNPE) primer.

The SNPE primer of interest was attached to a polystyrene 384-well plate (NUNC). Briefly, 20 µL aliquots of 0.25 µM SNPE oligonucleotide in 50 mM N,N-dimethyloctylamine hydrochloride, pH 7.0 (ODA; Segma-Aldrich, Milwaukee, WI) was added to each well and incubated overnight at 37°C. The plates were washed with TNTw (10 mM Tris-HCl, pH 7.5, 150 mM NaCl, 0.05% Tween-20) three times and once with 1xTE/ISOH (10 mM Tris-HCl, pH 7.5, 150 mM NaCl, 10% isopropanol). The plates were incubated upside down at 50°C for 30 minutes prior to storage in sealed pouch with dessicant. 15 µL of the exonuclease digestion product was added to the appropriate well and the single-stranded PCR product was allowed to hybridize for 30 minutes at room temperature. All wells were subsequently washed with TNTw three times.

An exonuclease (-) version of the Klenow Fragment of *E. coli* DNA Polymerase I (United States Biologicals, Swampscott, MA) was used for template-directed single nucleotide extension of the SNPE primer. Briefly, the enzyme was diluted in a buffer containing 10 mM Tris-HCl, pH 7.5, 5 mM DTT and 0.5 mg/mL BSA. The extension reaction was performed in 20mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 25mM NaCl,10 mM $MnCl_2$, 15 mM Sodium Isocitrate, 1.5 µM each of the four 2', 3'-dideoxynucleoside 5'-triphosphates (ddNTPs), ddATP, ddCTP, ddTTP, ddGTP. Two of the ddNTPs were unlabeled, one was labeled with biotin, e.g. 2', 3'-dideoxyuridine 5'-triphosphate (biotin-ddUTP), and one labeled with

fluorescein, e.g. fluorescein-labeled 2', 3'-dideoxycytosine 5'-triphosphate (fluoresceinated-ddCTP). The determination of which labeled ddNTPs to use depends on the nucleotide identity of the presumed SNP. For example, a suspected C to T mutation can be assayed using a mix of ddATP, fluorescein-ddCTP, ddGTP, and biotin-ddUTP. The enzyme concentration was 0.02 U/μL and the reaction was performed at room temperature for 30 minutes. The plates were washed with TNTw three times, then 0.2N NaOH, and then three times with TNTw.

Detection of the extended primers was performed by standard ELISA techniques using two nucleotide-specific labeled antibody conjugates. The dilutions of each are determined empirically for each antibody lot to achieve approximately equal intensity for the two colorimetric signals in the presence of both alleles. Briefly, the wells were incubated for 30 minutes at room temperature with 10 μL of 1% fraction V BSA (Sigma, St. Louis, MO) in TNTw containing an alkaline phosphatase conjugate of antifluorescein (1:2000 dilution) (Boehringer Mannheim, Indianapolis, IN). After washing with TNTw six times, the presence of alkaline phosphatase was determined first by the addition of 25 μL per well of a 1.5 mg/mL solution of p-nitrophenyl phosphate (Moss, Pasadena, MD) in 100 mM diethanolamine, pH 9.5, 20 mM $MgCl_2$. The plate was immediately placed in a microplate reader (ICN, Costa Mesa, CA) and the development of color monitored spectrophotometrically at a wavelength of 405 nm after 24 minutes in an endpoint assay. Next, the detection of biotinylated-ddNTP was performed. The wells were incubated for 30 minutes at room temperature with 10 μL of 1% fraction V BSA in TNTw containing a horseradish peroxidase-conjugated antibiotin (1:500 dilution) (Zymed, San Francisco, CA). The plates were then washed three

times with TNTw and the presence of fluorescein was determined by the addition of 25 µL of a 1 mg/ml solution of tetramethylbenzidine (TMB; Moss, Pasadena, MD). The plate was immediately placed in a microplate reader and the development of color monitored spectrophotometrically at a wavelength of 620 nm after 24 minutes in an endpoint assay.

A scatterplot of the raw data of $OD_{405}$ v. $OD_{620}$ was used in the visual determination of sample genotypes. A polymorphism is identified when three distinct clusters are seen in the positive regions of the scatterplot. These correspond to individuals that are homozygous, forming one cluster that is positive for $OD_{405}$ and another that is positive for $OD_{620}$, or heterozygous, forming a third cluster that is positive for $OD_{405}$ and $OD_{620}$.

Figure 3 shows a scatterplot that was classified polymorphic. The PCR primers used were oligonucleotides of SEQ ID NOS:25 and 26 (Ref No. 261, Table 1). The SNPE primer used was an oligonucleotide with SEQ ID NO:27. The targeted nucleic acid with the suspected polymorphism contains the sequence of SEQ ID NO:28. SNPE was performed using fluorescein-ddCTP and biotin-ddUTP. The Y-axis corresponds to signal obtained from ddUTP incorporation and the X-axis corresponds to signal obtained from ddCTP incorporation. Note that there are clusters where each allele tested is positive (CC or TT) and where both alleles are positive (CT). This is an example where a SNP is identified. Note that there is another cluster about the origin which corresponds to no signal (NS) due to PCR failure.

Table 1 lists the invention oligonucleotides disclosed herein. Each row provides two PCR primers used

to amplify the target DNA comprising a certain SNP (Columns 1 and 2), one genotyping oligonucleotide (Column 3; referred to as a SNPE primer) used to probe the identity of the base at the location in the sequence corresponding to that SNP), and sequence of the region flanking the site of that SNP (Column 4). A "P" listed to the right of a PCR primer denotes a phosphorothioation of that primer at its 5' end. In this embodiment, such a phosphorothioation refers to the five most 5' nucleotides of one of the two PCR primers being linked by four exonuclease-resistant phosphorothioated linkages (e.g., 5' C-(p)-G-(p)-C-(p)-A-(p)-GTCTCAGGCCAGCT 3', for SEQ ID NO:2, where "-(p)-" represents a phosphorothioate linkage). While phosphorothioation sites are listed for the specific residues herein, it is understood that other modifications which confer exonuclease resistance can serve as equally desirable substitutes.

In this particular embodiment, nucleotides labeled as "X" refer to C3 linkers placed in the corresponding sequences at the location of the X. While C3 linkers are listed herein, it is understood that other single-nucleotide-spacers can serve as equally desirable substitutes.

The sequences of Table 1 are arranged in the same manner as the SEQ ID NOs are listed. Accordingly, the nucleic acids of SEQ ID NOs:1, 2, 3 and 4 correspond to the nucleic acids in Row 1, Columns 1, 2, 3 and 4, respectively. Similarly, the nucleic acids of SEQ ID NOs:5, 6, 7 and 8 correspond to the nucleic acids in Row

2, Columns 1, 2, 3 and 4, respectively. Therefore, a general formula can be established to describe the SEQ ID NO of each nucleic acid:

SEQ ID NO= (4 x (Row Number - 1)) + Column Number

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Planking sequence |
|---|---|---|---|---|---|---|---|
| | | | - | | - | | |
| 1 | 255 | TTGAAATGTGAATAGTAAACTATGTAGAGATGA | | GGCAGTCTCAGGCCAGCT | P | CAGTATGGGAAAAAAGCAXCTCGGGAG | GTATGGGAAAAAAGCAGCTCGGGAGCTAGGGTGCTGAGCAGAGAAGAGTGA |
| 2 | 256 | CTCTTGGCTAGTTTATGTGAGATGAGA | | AGCTTTCAATCCTTCCAAACTTG | P | TCCTACTTCATCACTTCTTCTATTA | TCCTACTTCATCACTTCTTCTATTACGACTAATGTCTTCTGATGTTTACCA |
| 3 | 257 | CTACTGACTGCTTGACTGAGCTAATTAAT | | AATACATCAGAACCCCAAATCACA | P | GCTTGXCCTCTTGTCATAATCAGCC | GCTTGGCCTCTTGTCATAATCAGCCCGAGCGGGGATAGCTCACAAGACCAT |
| 4 | 258 | AGTTATTGCTTTCGTGAGGTGAAG | P | TCAAAGGAAAAGGTATGTGGAATATT | | AAGTGCATCGGCCTTCAGAACGAGG | ATTTTGCTGTAGTAATCTGTTGCACACCTCGTTCTGAAGGCCGATGCACTT |
| 5 | 259 | ATCTCAATTCCACGTTTGCTCT | P | CATGGAGGGAAAATCCTTAACTTT | | CTTTGCGAACAGAGGTCCCTGGAGG | AGGGGGAGCCTCAGCTCCACTGTCTCCCTCCAGGGACCTCTGTTCGCAAAG |
| 6 | 260 | AAGCAGCTCTGACTTTTGCAGT | P | CCCCTGGACCATAACTTCAGT | | GTGTTXCACATAAAGTCAGCACATTTT | CTGACTTCAAGACGTCATTGATCTTAAAAATGTGCTGACTTTATGTGCAAC |
| 7 | 261 | GTGGATATAGTAATTATCAGACATGGACATTA | | ATTTTATTGTTTTGTGGCTCTCAGTT | P | ATTTATTCAAGAAAXCAGATGATAAGA | TTATTCAAGAAATCAGATGATAAGACAGAGGACTTCAGCATAGAACTGAGA |
| 8 | 262 | CGAGCATCAGGTTATTGAAGC | | CTAGGGAGTTAGCCCCGCT | P | CAGAGAGGCCTGTGAAGAGCTACCC | CAGAGAGGCCTGTGAAGAGCTACCCGTGGATGCAGTGAGTGTGGGGGTAGA |
| 9 | 263 | CAAGTGAGTAAGGGGCTTG | | CTCACATCAGCCTTCTCCATC | P | TTAGAACACTGGGGGATTTACCTTG | TTAGAACACTGGGGGATTTACCTTGCACTTTTTAAAAATAAGACTCATGAT |
| 10 | 265 | TGAAGGAAGGCGGCTGCA | P | GAAACTCTCTTTCCCACAAAGGA | | CAXAGXAGGGTCTCCTTTTTCTACTCC | CAAATACTTTGAGTGCTGCATCTTTGGGAGTAGAAAAAGGAGACCCTCCTT |
| 11 | 266 | GTGGTGGAGTCAGGACATGAGTA | P | ACACCAAAGGGTTTTTGTGATAATC | | AATGAGATAAGGGCTATXAAAAGTTTA | AATAACTTATTTTGCAAATATTGTACTAAACTTTTAATAGCCCTTATCTCA |
| 12 | 267 | TATTTGCCAAACCTTTCGC | | GAAAAAAACCAAAGGGGTGC | P | AATACCACACTATTTGATTCCTGTAGCTT | AATACCACACTATTTGATTCCTGTAGCTTCAGAGTAAGTCTTGAAGTCAGG |
| 13 | 269 | AGTGAAAAGGATCRGTCACAGC | P | CATATAAATCAGGAGCAGAAWCAGAGA | | CAGAGAAGGCCCCCAAACTCAGACA | AAAATGTTTCTGATGTGAATTTAAAGTGTCTGAGTTTGGGGGCCTTCTCTG |
| 14 | 270 | AGGATCRGTCACAGCAATAACTTAAG | P | AAACTCAGACAYTTTAAATTCACATCAGA | | TTCACATCAGAAACATTTTGCCACT | AATGGACATATGTATCCTAAGAAGACAGTGGCAAAATGTTTCTGATGTGAA |
| 15 | 271 | ATGGTTTAAAAGTGTGTGGGACTTC | | CATGGCAGAAGGTGAAGGG | P | ACTTTTGCTCACTCTCTCTCTCCTG | ACTTTTGCTCACTCTCTCTCCTGCCACCATGTGAATAAAGTGTTTGCTT |
| 16 | 272 | TGACTGGCAGATTGACAAAGAA | | CTATGGCGCTGCATGGCA | P | AGTCXTCTAAATGCATGAGGGTGAAGC | TCTTCTAAATGCATGAGGGTGAAGCGTGGGAACTGCTGTAACAGGCCCCAT |
| 17 | 273 | TGTACCTGCTTGTCATATGCTGAT | P | GTTACTGATGGAGGGGTGGATATAC | | ATAGATGGATGGATGGATAGATGGA | CATTCACCTGTCTTTCTATCCTTCCGTCCATCTATCCATCCATCCATCTAT |
| 18 | 274 | GAACTTGATTTCCTATGTGAACCTTATATT | | TCTATTACTATTTATGCACTGGAATACTTCTATAA | P | TTCATTTACAGTAATTTTACAGTTGATGGGGGAATATATTTTTTATAGAAGTA | CATTTAGAGTAATTTTACAGTTGATGGGGGAATATATTTTTTATAGAAGTA |
| 19 | 275 | AAATTTGGGTGGGGACACA | P | CTAAGATATGGAGCAGGTACCCC | | ATGCAAACCCTCCACAACAACAAAA | ACCGTATCACTTAACAATGTATGCAGTTTTGTTGTTGTGGAGGGTTTGCAT |
| 20 | 276 | GTGGAACAGAATAGAGAGACCAGAAA | P | TGCAAGTGTGTGTCCAATAGTTCT | | TTGTTCCATTGTATTGTGCCTTTTC | AATGTAAATATAACCAAGTGATCTTCGAAAAGGCACAATACAATGGAACAA |
| 21 | 277 | ATATAATCATTCAGCAGATATTTATCGATTG | P | GCTGGATCAGGGCTCCTT | | TTGGGTGCCCACTAGCCTTGCCTTT | TAATAAGAATAAAGGAGGCTGTGATCAAAGGCAAGGCTAGTGGGCACCCAA |
| 22 | 278 | TCCTATGATCTTAAACTTCCCTGTACC | P | CAATGAAATGGGTATGAAAGTGCT | | GTGCTGTATGATGXCACTTCTGGGCGT | CTCTGGATTTGAGGTTTGCATGGGTCACGCCCAGAAGTGGCATCATACAGC |
| 23 | 279 | GGGTTTACATTTGTGCTTAATCAATAT | P | TGGGAATAGATACGCCCACA | | ATTCAGAATTTACTXCTACAGCACAAT | CAGCATATGTTGTTTAAATATAATTGATTGTGCTGTAGCAGTAAATTCTGA |
| 24 | 280 | GATCCTACTTTGGGACCAGGT | P | CCAGGAGTGGAAGAGATCGC | | GAATTTTTTXATTGATTATACACTATA | TCTATTGTACCCTCCCATGAAGCCAGTATAGTGTATAATCAATTAAAAAAT |
| 25 | 281 | CTAGTTCTTTTGGAAAAGATAAGCCAA | | TCTTCACCCTAGTTTGCACAATTC | P | CATGACTCTTAAGTGGATGAAAGTT | CATGACTCTTAAGTGGATGAAAGTTGAGTGTGCAGATGTCTGCATGAATTG |
| 26 | 282 | ATTAAGTGCCTCACGTAATACTGGG | | CTTCGGCCTTCTCAGGGC | P | TGGGACGCTGGAGAGACACAAGGAA | TGGGACGCTGGAGAGACACAAGGAAACCCAAGATTATTTACTAGCCTTAAT |
| 27 | 283 | TGGGGTTACAGAAACTTACCATTACA | P | ACCACTGCACTCCAGCCTG | | AAGTGTGACTCCGTCTCAAAAAAAA | AAAGATGTTTTATTGTTTTTTTTTGGTTTTTTTTGAGACGGAGTCACACTT |
| 28 | 284 | TGTGACTGGCTAAATCACTTTGAG | P | CCAGATGGATTTTCTGCACC | | CACXAGGACTTGAAGTCTTGGAACATC | TGCAAGACTAGAGTGCTTCCAGCACAGATGTTCCAAGACTTCAAGTCCTGG |
| 29 | 285 | AGCAACCAAAAAAAAAAATGTGTAGA | | CTAAGAATGGAAATCCTGCCCT | P | AGGAAAAGCAAACGGATATTGTCTG | AGGAAAAGCAAACGGATATTGTCTGCGTGTAGAGCCGTGGGGCCACTAGGG |
| 30 | 286 | CTGGGGCAGAGGCTAAACA | | CAAAATACACATACCTTTCCCAGTAAC | P | TTGTTGCTTCAAGCCAAGAACCTTA | TTGTTGCTTCAAGCCAAGAACCTTACGGCTGGGTGAAAATTCAAGACTCTG |
| 31 | 287 | CCATTTCATGTGCTAAAAACCAG | P | TTTTGGAATTTTTCATAGTGTTCCC | | TGTTCCCAAACTTGAYACTCATAGG | ATCAAAGTAAAACCTGTTACAAATAGCCTATGAGTRTCAAGTTTGGGAACA |
| 32 | 288 | TCAGCCATGATTGTGAGGC | | TGCTATAAAGACATACCCAAGACTGG | P | ATGTGGAACTGTGAGTCAXTTAAACCT | GTGGAACTGTGAGTCAATTAAACCTCTTTTCTTTATAAATTACCCAGTCTT |
| 33 | 289 | CTCACCACCTACAACTTGRTATTTAGC | P | GTATTTCTCATCTAAATGAAAGCACATTTT | | AAAGCACATTTTTAAGAGAGAAAGA | ACTTTAATATTTCTATATCTTACACGTCTTTCTCTCTTAAAAATGTGCTTT |
| 34 | 290 | CAGAAAAATAGAAGCAATAGGACAGAC | | ATATGGTGGGTGGGACTTAGC | P | CTATAGATACAGATGATATTTATTA | CTATAGATACAGATGATATTTATTACGGGAATTGGCTCATGTGATTATGGA |
| 35 | 291 | ACCTCATGCATTACAAGGCTCTT | | GAAAGTTGGCAGGTACAAGGTCT | P | TCTGGTTGCACCXCCATXCCCTGGGCA | TGGTTGCACCCCCATCCCCTGGGCACGTGAGAAATTCATGAGCCCCATTCT |
| 36 | 292 | GCTACCATCTTCTTTGGCTATCATT | P | TCAATGTTATCGATCAATGTGTCATAG | | AATGCXCAAATGGTATGAGTGTGTGTT | GAAAATGCTCTATTCATTAAAACACAAACACACACTCATACCATTTGAGCA |
| 37 | 293 | GGGCTTCAGCAAAATACAGGT | P | CCGGGGATCTGAGTGACA | | TGGTAAAAAAXGATTTCATTGTGATTA | TGAAAGAGACATCAAAAATTTTAACGTAATCACAATGAAATCATTTTTTAC |
| 38 | 294 | ATTCAGTCCAGGGCTGGG | P | GCCATCTAGCATGAACACATAGC | | ATAGCCATGAGCCATCAATGAGTCC | GTCACTGGGAAAGACAACCTCCAGCCGGACTCATTGATGGCTCATGGCTAT |
| 39 | 295 | CTTCAAGCCTCCACTACATCCTC | | AGGTAGGAGAAACATGAGAGTTTTTTTAA | P | TCCAATTTCTTGATAAACATGCAAC | TCCAATTTCTTGATAAACATGCAACGTATTTTTTTCTGAGAAAATAGAAGC |
| 40 | 296 | CATGGGGAGAGAGAATCTAGTAAGTG | P | TCCAGAGGCAGTTCAGAATAAAAA | | AAAAAAATXATGTGTTGATTAGAGACT | AACAAATATGTGTCTGTAGCTGCAGGAGTCTCTAATCAACACATTATTTTT |
| 41 | 297 | GCATCTTGTTTTGAGATTCCATG | P | AGAGGGAATGATCAGTCAGGG | | GGGAAATTCATCTXTAGACATTCATTA | GGAAAGTGACAAATTGCAAGGAAACGTAATGAATGTCTATAGATGAATTTC |
| 42 | 298 | CTCACAGCACCTCAGCACC | | GTATACCAGGCAAGGTAGAGAAAGG | P | AAACCCCCTCTATCCTCAGTGTGTC | AAACCCCCTCTATCCTCAGTGTGTCCCCCAAAATAAGAAAAAAATGTTTTAT |
| 43 | 299 | AGCACCTAAACCCCCTCTATCC | P | CTGGGAATGGAAGAAAGCAGA | | CAGACTTTTAAGXATGTTTGCCTCATA | GAAAAAATGTTTTATAATGAGCACACTATGAGGCAAACATGCTTAAAAGTC |
| 44 | 300 | TACAGGGGATTTTGGATCTTTGT | P | GTTTAATCCTCAGAACAATCTCTCCTACT | | GGCAGAAGTGGCCCTATXAAGACACAT | AGCTTATCTCCCACTTTCTGGCATGCATGTGTCTTAATAGGGCCACTTCTG |
| 45 | 301 | TTGATCTTACTCAGCTCTCTTCAGAG | | ACCCTGATTACAAGGGTTATAAAGAAG | P | AGATCCAGCTTAGATTCCCATTCCA | AGATCCAGCTTAGATTCCCATTCCACCTGCTGTCTCAGTATTCTTCTTTTAT |
| 46 | 302 | TTAAAATGCAGACACTTCTTAATATATCGG | P | TTTTAAGATTTTCAGAGGCAGGTTC | | CAGGTTCTGAATAGCCTTTGGTCTA | TCTCAGTCATGAGGCTAAATTAGCCGTAGACCAAAGGCTATTCAGAACCTG |
| 47 | 303 | AATAGAACAAAGGAAGTTTGATGTGG | | GAAATGACTTGCGTAGGCCA | P | AACCCXTTAGCAAGACAAAGATTTCTG | CCCTTTAGCAAGACAAAGATTTCTGGACGTGAGTCTGCCACTAAGTAGCCG |
| 48 | 304 | AATTGAGGATCTAGAACAGCCCC | | GTTTGATTCCACATGTAGAAAGGATG | P | CTAXTCCXACCGCAGAGTGGACTTGGT | AGTCCCACCGCAGAGTGGACTTGGTCTCCTGGCCAATTGCAGGCAATGAAA |
| 49 | 305 | CTCCTATGTCTGGGAATTAATAGTAAGAAA | | TCAATAACACATTTGCCTAAGTTCCT | P | ATTTTAAATGAGTATTGATGCAATA | ATTTTAAATGAGTATTGATGCAATAGTTGTTATGGAATATATTAAGGAACT |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 50 | 306 | TAAGGTGGGCACTGAGCATG | P | GAATGTGCCRTTTTATTACATAGGTATACA | | CCACGXTGGTTTGGGGXTCACCTCTTT | AGCCCACCTAAGAGARGAATCATGGGAAAGAGGTGATCCCCAAACCACCGT |
| 51 | 307 | TACCAGAAAAGTGGGACATTCCT | | CTTCTGAGCCCTCCAAACTGT | P | TGAAGATACCTGAAAATGTGGAAGC | TGAAGATACCTGAAAATGTGGAAGCAGCTTTAAAATTGGGTAAGGAGCAGA |
| 52 | 308 | TTTGATGTTTGTGACCACTGCT | P | CTATTGAATTGAACATATTTTATGGCTTC | | TGGCTTCGTGGCTTTGTGACCTTGT | TTCCCACAGGTTGCTGTTTGACCACGACAAGGTCACAAAGCCACGAAGCCA |
| 53 | 310 | AAATATACAGACACAGTGGTTACTGGTG | | GTGATGGGATTATAGGCATGAGC | P | GGGGAGGTAGAACAGAGGATACAAA | GGGGAGGTAGAACAGAGGATACAAAGTAGCAGATATAAGGCACTGTGGCTC |
| 54 | 311 | GTGGGACCTAATTAAACTAAAGAGCTTC | | TGTCTGATGCACAGTTTGAAAATATT | P | CAAAATAAACTACCAACAGAGTAAA | CAAAATAAACTACCAACAGAGTAAACAGACAACCCACAGAATGGGAGGAAA |
| 55 | 312 | TTTTCACTCATATGGGAAAGCTAAAC | P | CAATTAACCTTCTCCTCTCTCTCCC | | CTCTCCCCTCTCCCCACCATCCTTC | GTAGATTGATGGTTACCAGAGGCTAGGAAGGATGGTGGGGAGAGGGCAGAG |
| 56 | 313 | GGCCACACATGATTCTTTACATG | P | TGATCTGTACACATCCTGGGTTC | | TGCCTGGAATTGATTTTTGTATATA | ATATGAGAAAAATTTAAAATCAATTGTATATACAAAAATCAATTCCAGGCA |
| 57 | 314 | GCCAGATGCCTTCCTTAGTAACTT | | GTGAAATAGTAAATAGTTAGACTAAGATGAATGCA | P | GAATTTTGCGCTGATTATAGAGTGT | GAATTTTGCGCTGATTATAGAGTGTGGAATTGATTGCATTCATCTTAGTCT |
| 58 | 315 | CTTGCAGTAAAGAAGAGCTTTGTAAAG | | TCTACTGGAGAGCGTTGTTCTGT | P | GCTTGATGTCTTAGTTACTTTCATT | GCTTGATGTCTTAGTTACTTTCATTGTTGGATCTCAGTTTTCTGAGCACAG |
| 59 | 316 | TTGCCACCTGGACACTTTG | P | AGTCTGGGTCAATCACCCC | | CAGCCAACACTGTAACTCCTTTCTT | CTCTTCCTTCCTTTAAATCAACAGGGAAGAAAGGAGTTACAGTGTTGGCTG |
| 60 | 317 | AGAAATTCAAGCCTGCTGCA | | CTCCTACAACAAAAACACACTTAAGCA | P | TTAACTGGTTGTTTTGTAGATTTTA | TTAACTGGTTGTTTTGTAGATTTTACTGTATATTGCTTTATATTGTCTGTA |
| 61 | 318 | TCCTTAAAAGGAAAGCTCCCAG | | CTGCTGGGTACACAGGGTG | P | ATCATTAGCCAGTGTTTATTTGGCC | ATCATTAGCCAGTGTTTATTTGGCCGCAGGGCAGGAGCAGGCCCTATACTG |
| 62 | 319 | CTTGTATGAGGAAGATTCTGGGTTAC | P | CAGTACAGCAATAAAAACTGTTCTGG | | CAGGTCCACCACAGAGTCTCATTCT | CTGAGTTCAGTCCAGACATAACAGCGAGAATGAGACTCTGTGGTGGACCTG |
| 63 | 320 | TTATTCTACCAAAAAGACATATGCACTTG | | CTAATAATACTGTGTGGATGTACCACATTT | P | GAGTCAGCCTAGGTGCCCATCAACA | GAGTCAGCCTAGGTGCCCATCAACAGTGGATTGGATCAATAAAATGTGGTA |
| 64 | 321 | AGAAGTACTGGGATGATCTTTGGG | | GCAAAGAGCGAAAGAACAAGC | P | TGATGAAAGAGAGTTGACTTGGGGG | TGATGAAAGAGAGTTGACTTGGGGGGCAACCTGCTGGGGTCCCCTTCCATT |
| 65 | 322 | CCGGGGATCTCAAAAACCT | P | GGAACAGGATGGATATTTTGGG | | TTTTTAAGTTTGTAGGACTGTTTGT | GCAGTTTAGAGGTCCTTAATGAATCGACAAACAGTCCTACAAACTTAAAAA |
| 66 | 323 | GTGTTCCAAGAACTTTATCAGCATC | P | AGTTTTTGTTTCCTGATTCATAGTGG | | AGTGGGACTAATAATACTTAACCTC | TCATTATGCTGCCACTAGAACTTAAGGAGGTTAAGTATTATTAGTCCCACT |
| 67 | 324 | AAATCTTATTCCTCCCCCTCATG | | CTTATGCCTAGTTTCTTCTCCTAGTTTCA | P | ACTATTAGTGATTCCAGACTTCATT | ACTATTAGTGATTCCAGACTTCATTGTCTCCCCTAGGTGGGAATGATTTAT |
| 68 | 325 | TTCGTGTTTTACAAAGCATGAGC | | ATTCTGATGCTGCTTCAGTTTGA | P | GGAAGCATGAGGTTGTCCAAGCAGG | GGAAGCATGAGGTTGTCCAAGCAGGCCCTGGGGCCAGGACAGAAGAGAGGT |
| 69 | 326 | GTTCCCTGTTAGAATACACCCACC | P | AGACCTGGTTCATACTGATTGATAGC | | TAATTTAAAAGGAAAAGACTCAAAC | AATCAACAGGGAAATATTACACCTAAGTTTGAGTCTTTTCCTTTTAAATTA |
| 70 | 327 | CATATCGCTGAAGTGAAAGTCAGG | | CAAAAAGCTCAACGAAATTTGG | P | CTCXAAGXAATGGAATGGGGATATTTC | CCAAGAAATGGAATGGGGATATTTCGGTTGGCTCAGATGAATCTGAGAATC |
| 71 | 328 | CTGGATGTGTTTCAAACAGTGAGA | P | AGAGGGCAAGAAGGAACACAG | | CAGAATATTTGAGAGAGTAGGAAAA | AAAGAGGCAGTATCCATGAGCCTGAATTTTCCTACTCTCTCAAATATTCTG |
| 72 | 329 | TGGTCTTGAACTCCTGGGC | | CAATAAGAAAATGAACAACTCAACTTAAAAG | P | CAAGTGATCCTTCTGCCTCAGCCTC | CAAGTGATCCTTCTGCCTCAGCCTCCCAAAGTACTGGGATTGCAGCATGAG |
| 73 | 330 | CTGTCTTTTTTTCTAATCAGTTTCCTTC | | ATTTGGCGTTTGATAATCCTCA | P | ATAATTGATATCAGATGAACACAAAG | ATAATTGATATCAGATGAACACAAAGCACATAGAWACCTGATGTTTCTGAG |
| 74 | 331 | ATCTAATGCTTACCATGTCTTCATGG | P | CCTTGGTATGTTCACAAACCTTTG | | GCCTGCCCTGTAGGACTTACCTGAC | GGCTACTCAACGTCTGATTTGATAGGGTCAGGTAAGTCCTACAGGGCAGGC |
| 75 | 332 | TGGAGTAAGTAGGGGTTGCACA | P | AATAAATTATTTGGATAGCCAAACTTGG | | AAAGGTGTTTCCACCATTGATGATT | CAAGGCATCTTTACCCTTGATGATAGAATCATCAATGGTGGAAACACCTTT |
| 76 | 333 | CCAGGTGACCAGGCCCCA | | GGCAATTGATGGGCAAGTG | P | XCTAGCAXCCCAAGCAGAGGCAGCA | CCTAGCAGCCCAAGCAGAGGCAGCACTCCCTCCCCTGCAAGAACAGCCTGC |
| 77 | 334 | TTGGAACTGACTAACAGGCCA | P | CAACTATTTAACCAGTCGCCAAAA | | TTCACGTTCCAAACTTTCCCCGACT | TTGGAAGGCTTGGAAGAAGACTCAAAAGTCGGGGAAAGTTTGGAACGTGAA |
| 78 | 335 | ATCTCTGCACTCTCATGTTCATTT | P | GTGTGTGTGTGTGTGCGC | | CTGTCAATGTATGTTTAGTTTGTTT | AGCATTACTGTAATAGCCAAATATGGAAACAAACTAAACATACATTGACAG |
| 79 | 336 | GTAATATCATTAGGCACCCAACTAACAT | | GGAGAGATGTGAGGTTTGAATTTC | P | GTCAGAACTGTATGTTGATACTTGC | GTCAGAACTGTATGTTGATACTTGCCTTCAGACAGTAAAACTAATTTGAAA |
| 80 | 337 | ACTGCCAGTGGGTTGTTGAA | | TAAAGGGTAAAATCCAACAAGAACAC | P | TTGATGTTCCAGTGTTGGGTGCATA | TTGATGTTCCAGTGTTGGGTGCATAGAAATTTAGGTATTTAGGCTAGTTAA |
| 81 | 338 | CCGGGGATCTGACTATCTTGT | P | CATAACATGGACACTGAGTATAATATCTCC | | TACAGTCCATCAGTGAAATAATATG | ATACATATTTAGGGACTTTTAACACGCATATTATTTCACTGATGGACTGTA |
| 82 | 339 | ATCTAGAAATAGAACAGCCTGAATCTGTAA | P | GAATGGGAGTACTAGCCATCACC | | ACTGGATCTCTATCTTCTXAACAGCCT | GTCAGTTGACAGCAGCTGCATTACGAAGGCTGTTAAGAAGATAGAGATCCA |
| 83 | 340 | AGTGAGTGAGGTGCGCTACAG | P | CAATGGCAGTATTGGTGTTATGC | | ACTTGACTGCAGGTTCATTGAGGGC | AACACAGTTGAAAAGAATCTGACTTCGCCCTCAATGAACCTGCAGTCAAGT |
| 84 | 341 | CGGGGATCTTTCTTAAAACCAT | P | GTAAAATGATTAGATGTACTATTTAAGGAGTGACT | | CTCCGAAATAAGCAGAAAACTAACA | TATCTATGATAATTTGGAGACAAACGTGTTAGTTTTCTGCTTATTTCGGAG |
| 85 | 342 | CAACATGGTGAAACCCCATC | | CACCTCCCAGGTTCAAGAGAT | P | AAAATTAGCTTGGCGTAGTGGTGGG | AAAATTAGCTTGGCGTAGTGGTGGGCGCCTGTAATCCCAGCTACTCAGGAG |
| 86 | 343 | TCACTAAGACAGTCACAGTCAATTAAA | | TTGGTTCAGTATTATAAATTGTTATTGGAAG | P | ACTTAAAAAAAAGAGAAACAAAAGGA | ACTTAAAAAAAAGAGAAACAAAAGGACGTGTCAGGACAGCTTCCAATAACAA |
| 87 | 344 | TCCCATGCTCTCTGTTTCC | | GGGTTTGGGACTCCAGGA | P | CTGGGAAGCCAAGXTCATCAAGATCAT | GGGAAGCCAAGATCATCAAGATCATAGTCTTCTTTTGCTCACAGCACACCC |
| 88 | 345 | TTATATAAAATTCTGGATACAGGCTCCC | | CCTACCACTTTCCTCATAAGCCA | P | GCAGGCCTTGAAAATGGAAGTTTAC | GCAGGCCTTGAAAATGGAAGTTTACCATTTTCAACCGAAAGAAGGCTGGCT |
| 89 | 346 | CTGAATAGAGATTGGGGAAAAAGAA | | TTATATAACTCTTTCTCATTTTTCTGGCTTT | P | GGCAATTGGGGGTGGTCTGGAGAGG | GGCAATTGCGGGTGGTCTGGAGAGGGTACATTTAAACCAAAGCCAGAAAAA |
| 90 | 347 | GCCCTGGGAAGAAAGACAAC | P | TTTTTCCCCAATCTCTATTCAGTTAC | | TCAGTTACCCTTTCTTATTTCTTCA | GTAATTTTAGTTTGTGGTAAGTACAGTGAAGAAATAAGAAAGGGTAACTGA |
| 91 | 348 | AAACTGTTCTTGGACTCAGGCA | P | CATTTAATCTGCATGACAATCCC | | AGCCTGTGCCAGTCTXAAACTTGCCTA | ACCCAACACATAATCTGGCACCTTCCTAGGCAAGTTTAAGACTGGCACAGG |
| 92 | 349 | GAGGACACATACTGTCATTGGATG | | TGTACTTAGCATACAAATCTCTAGGATGATT | P | ACAAGCCAAATATGTTACTAGAAGT | ACAAGCCAAATATGTTACTAGAAGTAATTAATCTATTCATTCAAATCATCC |
| 93 | 350 | CCRTATTTCTAACAGGAAAATAGTCATTTTA | P | AGCTCCCCATACCTGTTTGC | | AGCTGTATAATAGAGTGTCTCATAC | TAAAGGTCTGATTTTTTACAAAGTGCCTATGAGACACTCTATTATACAGCT |
| 94 | 351 | GAAACTAATGAGAACAAACACACAACAT | P | TTTTGATGTGAACATTTAGTGCTATAA | | GCTATAAATTTCTCTCCTAACACTG | CCAGAATCTCTGGGACACAGCTAAGGCAGTGTTAGGAGAGAAATTTATAGC |
| 95 | 352 | GTGAAGATCGAATACCTAAAATTATCTTATTTAC | P | AGGTTTTGTTCCAACTCCAAGG | | TGGAGATTAACTCTTCACTGACTTC | ACATAGGTTAAGTTCATGCTTTCAGGGAAGTCAGTGAAGAGTTAATCTCCA |
| 96 | 353 | GCGGGATCTCTACAAGGAGAA | P | GTATTTTGATGGGAATTGCATTG | | TKTTTCCTTTTTTGTGTGTTTCATC | ACAMACCACTGCTGAAAGAAATCACCGATGAAACACACAAAAAAGGAAAMA |
| 97 | 354 | GCTGAAAGAAATCACYGATGAAAC | P | TGTATGCATTGCTTTGGGC | | CAATATGGTCCTTTTCACAATGATT | AACATCCCATGCTCATGAATTGGAAGAATCATTGTGAAAAGGACCATATTG |
| 98 | 355 | TCTGCTCACTCCAATTCTGGG | | GATTCCAGGCTGTCAGCTCC | P | CGAAAATTATTTCAGTCACATTGTT | CGAAAATTATTTCAGTCACATTGTTCGTAGCAACCATATTTTAAAGCACAG |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| | | | - | | - | | |
| 99 | 356 | TGAGGCAGGAGAATCACTTGA | | TTTTTTTTTTGAGATGGAGTCTTGC | P | ACCCAGGAGGTGGAGGTTXCAGTGAGC | CCAGGAGGTGGAGGTTGCAGTGAGCAGAATTCACACCACTTCATTCCAGCC |
| 100 | 357 | AATGGGCGCACTGCTGAG | P | CCTCATTTGTAAAACTGGCAAGTAA | | CAGAACCCAATGCATAGTGTTATTC | ATAGGAATCTCTTCAATTAGTCCTCGGAATAACACTATGCATTGGGTTCTG |
| 101 | 358 | TTAGGGCAAGGATAAGCCAGTAT | P | GTCTATAGCAGGTCAAATAWCTAGGCC | | GCCTAATCTTAGCCAGAGGGACCAG | GCTGTATTTGTTCCTTGCTGAGGGCCCTGGTCCCTCTGGCTAAGATTAGGC |
| 102 | 359 | TTGGCTTACTGCAATCTCTACCTC | P | GACCAACATGGAGAAACCCC | | CCATCTCCACTAAAAAAAAAAAAAA | ACCACCATACCTGGCTAACTTTTTTCTTTTTTTTTTTTTTAGTGGAGATGG |
| 103 | 360 | TTAAATGTTTATTGGCTGTCTTCACC | P | AAATGTAGACATGCATTCACTTAGGAA | | ACTTAGGAAATATTTATGAACATGA | CCCTATCAGAACTCCCAGCATGTAGGTCATGTTCATAAATATTTCCTAAGT |
| 104 | 361 | TAATATCCTGATGAATGAAGATGGCTA | P | CAATTAGCTCTGAAGAGTCAGCCT | | CCAGATACCTGACCTCCTATGAAAGT | CCTCATACCAGAAGATGCCATCAAGGACTTTCATAGGAGGTCAGTATCTGG |
| 105 | 363 | GAATTATTTTCTTTGCACTGTTAGGACA | P | CATAGTCATTTGGGGAACTGATATTG | | TTGTTXGAGXTTAAAAATCCAGCAAAA | ATCAAATGCCTAACAATTGGTAGTACTTTTGCTGGATTTTTAATCTCCAAC |
| 106 | 364 | TGCAAAGAAGATTTTTGAATCCC | P | GACTGGGTAATTTATGAAGAAAAGAGTTT | | CAGGAAGCATTACTGGGAGGCATCA | TCACCTTCGGCCATCATTGTGTGTCCTGATGCCTCCCAGTAATGCTTCCTG |
| 107 | 365 | ACCACCATGTCTGGTTAAGTTTTTAA | P | CATAATTCCAGCAACTCAGGAGG | | GGCTGAGGCAGGAGGATAGCTTGAT | TCCCAAGGTAGTCTCAAATTCTTGGGATCAAGCTATCCTCCTGCCTCAGCC |
| 108 | 366 | TACGTAATCATTATTTTTCACAGGCTG | P | GTCTTGGTCTCAAAGTAACCCAAA | | CXCAAAXCTTCCACCTGCCAAGGATGG | GGTGGCGGGATTAGCCTGACGCCACCCCATCCTTGGCAGGTGGAAGGTTTG |
| 109 | 367 | CTAGGCATGTCAAGTTCTTCATGG | P | CTTTATTCCTCCCTACCCTCATTG | | CTAATGATGAGGGCCAXTTCTCCTTGA | AGGAGAGAAGAGGGGTCTTCATTTTGTCAAGGAGAATTGGCCCTCATCATT |
| 110 | 368 | AAAATGCCCTGTCTAGAGGGAG | | CTAATCTCATTCCTCCTTTCTTCCTT | P | GCGCTGTGGGAATGTAGACTTCTTG | GCGCTGTGGGAATGTAGACTTCTTGGGGAAGATTTCCGAGTTGAGTAAGAA |
| 111 | 369 | TCCTCATTACATTTTAATGGCACTG | | TGCCCTGTCTCACCTGCA | P | AGTTACAAAATGAAAAAGACTAAAT | AGTTACAAAATGAAAAAGACTAAATGTTAGTAGAGTTCAGAAATCTGTGGC |
| 112 | 370 | TTGTGAGGCAACCCCAGTATAC | P | CTATACAGTGCTACTCTACTCACACCCA | | AGCTCCCCACCCGCACACACACACA | AGTTTCTTGATGACTTTGAGTGTCAGTGTGTGTGTGCCGGGTGGGGAGCT |
| 113 | 371 | TATGGWAGTGAAAGCAGAGTCTGG | P | CCAGATATGACYCCCCTCC | | TCCCCTGCTCAACXACTTGTTATGGCT | TCCATTTTAACCCAAAGGCAATGGGGAGCCATAACAAGTGGTTGAGCAGGG |
| 114 | 372 | CAGTTGTTGGAAACACTATTATTTAATGTACTAT | | GCAGAAGGATCTAACAGATGAATTTG | P | CCAATGAATTTACGGCACACTATCC | CCAATGAATTTACGGCACACTATCCGCTCTAATCTAAATTTTTGTGTATCC |
| 115 | 373 | CGGGGATCTGAAAAAAAAATTC | | AGAGCCAGCATTGTCTCACTTG | P | ACTTTATAAATGATTTCACTGCATC | ACTTTATAAATGATTTCACTGCATCCCCCAAAATTCAATCCCTAATTTACA |
| 116 | 374 | TCCCAGATAGTTCCAGAGACTTCA | P | CTTTAGCTTCAAGTTCAGAAGATGACTT | | CTTTTTACTATGTTTTTGTCCTCCC | ATGAGCACATGTGAGTGTATATGGGAGGGAGGACAAAAACATAGTAAAAAG |
| 117 | 375 | TCACAGAAAGATACTGGAGAGGGT | | CAAACCCCTAAGCCCACCTA | P | ACTTTGGGAGGAGTTTGGGGCTGTG | ACTTTGGGAGGAGTTTGGGGCTGTGCGAGGGTGACTCATTTTTACCTATGT |
| 118 | 376 | AGACTTGTTGATGGCTTTGACC | | CTAGGGCAAAATGCCACTAGTTT | P | GATGAGGAACTTGTTGGGAACTGGA | GATGAGGAACTTGTTGGGAACTGGAGTAAAAGTCACTCTTGCTAGGCAAAG |
| 119 | 377 | TATCAGTCTCTTGAGCTATGGGG | P | CCGAGGAGGGACCTTCAA | | AGAGCTCCAXATCCAGCCTCATTTCAC | GGTTCCAGGGCTCAGCTTCTTCATCCGTGAAATGAGGCTGGATTTGGAGCT |
| 120 | 378 | CTCCTGGTGTGGGCTTCTG | P | ATCTTGGCATTGAGAACAAGAAGA | | GAAGAACCAGGAGCCAAGGTGTGTA | AATGGCAGAGGGAAACCTCACCCAGGTACACACCTTGGCTCCTGGTTCTTC |
| 121 | 379 | CAGATTCACAGACTAGAAAGGGAGTT | P | ATCGAATTGAGAAGTAAATCGTGTG | | TCGTGTGCATGTACCTGTGTGTGTG | TCAGTAAAGTTAACCACACTCACACGCACACACACAGGTACATGCACACGA |
| 122 | 381 | TTTTTRGTTTGAGGCTTTTATAGCTG | | GCAACGCTGAGGGGAAAA | P | GCTAAAGATGTGCCTCAAGACACCC | GCTAAAGATGTGCCTCAAGACACCCCGATGTTAGATGCCTTTCCCAACACA |
| 123 | 382 | AGATGATGTGAGCTAAGGGAAGTCT | P | CTCTGTACTTATTATTCTCTCTACCTGGGA | | TAATCTCTCTGCCCTATTCTCTTTC | GAAGATGTGTAGAAACTACACAAGAGGAAAGAGAATAGGGCAGAGAGATTA |
| 124 | 383 | AAGACAGGGAATGTTTCTCTTATTTCTC | P | GTGAGTCATGTCCAGATGAAAATTT | | GAATTAXCAGACTCTTGCTXCATCCAG | GAGTTCTGGTCTTAATTATGCCTCACCTGGATGCAGCAAGAGTCTGCTAAT |
| 125 | 384 | CATGGAGACACCGGGTGG | P | CGAGAGATCTTTCAATTTCTGTTTG | | AATGACTACTGTATCCAGGCTTGAC | ATGGGCTGCAGGCATACATTCTGAACGTCAAGCCTGGATACAGTAGTCATT |
| 126 | 385 | GGGGATCTCAAAAAAGAAAAAAAA | P | GATCTCAGCTCACTATATCCTCTGC | | AGTGATTCTCCTACCTCAGCTTCCC | GCATGTACCTGTAATCCCAGCTACTCGGGAAGCTGAGGTAGGAGAATCACT |
| 127 | 386 | TATTTCCCCAAATTATCRTAACTCCA | P | CAAAAGAAAGAGTGCAGCGG | | CCCTTTACAAGCCAACTCTTCGTCT | CTTCTGTGGATTCCAGAGAGTAAGAGAGACGAAGAGTTGGCTTGTAAAGGG |
| 128 | 387 | CGGGGATCAGCCATTCAA | | TGAAAGTGGTCCTATCCACTGTG | P | ATTGAAAATATTATTATGTGAGGGC | ATTGAAAATATTATTATGTGAGGGCCGAAAAAGATGCAATCTGTACTCTCA |
| 129 | 388 | ATACTGTGAAAGATATGAGACTCTTGGG | P | CTTAAGAACTGGTCAAGAAAATCATGA | | AAATCATGACACTCTGGCTATACTG | GGATGGCGTGATACTCACAGCAACGGCAGTATAGCCAGAGTGTCATGATTT |
| 130 | 389 | ACACAGTGGGCMTGCTGT | P | AACAGAAAGGAACTCAGAATAAGCC | | GTATTAAGTXTAXATAGATTTTTTTTT | AATCCCAGGCTTTACTGGCAATAGTGAAAAAAAAATCTATTTAGACTTAAT |
| 131 | 390 | TTCGTGATACTTATTTAAAAGCATCTTTG | P | AGACATAGGACACAGACTGAATTTCC | | AAAAATAATACGXTACACCAATATCAA | GGTGATAAAAACATTAAGAAATATTATTGATATTGGTGTATCGTATTATTT |
| 132 | 391 | TATCGTATTATTTTTCCAGGGGATTC | P | ATTCAACAGTGAAGACAACTTTCACC | | ATGCTTATCTCTTGACTTCTTAAAA | GGATTTCTGAATATATTTTTAAATGGTTTTAAGAAGTCAAGAGATAAGCAT |
| 133 | 392 | AGTAGCTAAGACTACAGGCATGTGC | | CTAATACCAGTGCTTTGGGAGG | P | TTTTGTAGAGAAAGGGTCTTGCTAT | TTTTGTAGAGAAAGGGTCTTGCTATGTTGCCCAGGCTTGTTTCAAACTCCT |
| 134 | 393 | GTGACTCTTAGTGTGTAACAAAGTGCA | P | TACCTGCATAATAGAGCTTCAGTAAAAAC | | CXTCXGTAAAAACTATGGACACTGAAG | AGTATTACCATAGAAGCTTGCCTGAGCTTCAGTGTCCATAGTTTTTACTGA |
| 135 | 394 | CCCAAGTGTTACCCAAAACATACTAA | P | TCATGGATGCTGGGAGTTG | | GGTGTTCCTAGTTAYGGTTGCCAGT | GGCATTCTTATGTTTTTATTTGCTAGACTGGCAACCRTAACTAGGAACACC |
| 136 | 395 | AATGTCAAATTTAAGTGGGCATTCT | P | CTTCTTTGGCTTTGAGTCTGCA | | GCTGGGAGTTGGGTGTTCCTAGTTA | GTTTTTATTTGCTARACTGGCAACCGTAACTAGGAACACCCAACTCCCAGC |
| 137 | 396 | AATGGGAATCTTAGTGAGTTTGTTTCT | | GATTGGTTTCCAGAGGCATATTG | P | TCTCTAACTGGGCCATCTAATCCTG | TCTCTAACTGGGCCATCTAATCCTGCGCTTCCAGGTGTTCCTGGGGAGAGG |
| 138 | 397 | TTCGCAAGAGTGAGGGCTC | P | ATTTTCTTCCTCACACCTGATGC | | ATATACTTTCTGCCCCCCCTCCACTA | GGCAATGAGTTTGGCTTGCTGAGAGGTAGTGGAGGGGGGCAGAAAGTATAT |
| 139 | 398 | CTGTGTCACAGGCATTTGAGG | P | CGGTAACGGGGATCTGATG | | AAACCCTTCATGXTAAAAATCTAGCCC | CACACAKGAAAAGAGAGCTGAGATTGGGGCTAGATTTTTAGCATGAAGGGT |
| 140 | 399 | TCGGTACACCAGGGGATCT | P | CATTTAAGAACACCTGAGTTATGCTACA | | AAAGAAGATXCTATCTGTGAGAAAGCA | AATGACTTAAAAATTTTTTCTTCCTCTGCTTTCTCACAGATAGCATCTTCT |
| 141 | 400 | AGCTTACATTTCTGCATCAGTTCAT | | CCTTTTCAGACGGGCACTT | P | TCTTGGATCCATCCTCTGAAAGGTC | TCTTGGATCCATCCTCTGAAAGGTCGTTTCTTCTCCATAACACTCCTTGGG |
| 142 | 401 | ATGAGAACCCTGGAGGTATAGCA | P | CAATTTTGTCTATACATAATCTACCAAGCC | | CAAGCXAGTGATTTXCCTGGAATTATC | STAGTAATTGACTCTGAAACCCAAGCGATAATTCCAGGAAAATCACTGGCT |
| 143 | 402 | ATTATAAAGTCAGAGAGGTAGAAGGAGAACA | P | CTTTTGTCTGTGCTGCTCCTAACT | | AGTCCACTGTGCTCGGCTGTCTACT | AAATGAGGTGCTTTAGAAGTTACATGAGTAGACAGCCGAGCACAGTGGACT |
| 144 | 404 | CTTGATAGGCGGCTTTTACCTT | P | GACATAAAAATTGGATAGAAAGCATTTG | | AAGCATTTGATXTACAAGATTAAACTG | TCTGGTTGCATTGCAAGGTGGCCTCGCAGTTTAATCTTGTAAATCAAATGC |
| 145 | 405 | GTGGATACAGTTCAGATTCCTAACCA | P | TTATCACATGGGGACTACACCC | | ACCCCATCACAGTCTCATCTTATTC | TGGGAAAAAGTAAAAGATATGTAATGGAATAAGATGAGACTGTGATGGGGT |
| 146 | 406 | ATAGTGCACAGTCTTTATCCCTTTTTT | P | CTTTGTGGAGGAGGTAACTTCACA | | CAAATGGCTTXCTTTGGAGGCTTTATG | ACCCTGTGGACTGGAGCTAGGGGTGGCATAAAGCCTCCAAAGGAAGCCATT |
| 147 | 408 | GAACTGCAAAATCTCTAATATCTTATTTTCTG | | GGGGGAAGGGATGCTAATTAA | P | CCTCTGAGAAATGGGGATATGATGC | CCTCTGAGAAATGGGGATATGATGCCTATTAAGCTGAGATAATCAAAAATA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 148 | 409 | CCRCTGAATTTATATAGTACTTTTTTTTGG | P | TCCACCCAGTTCGAGCTTC | | CGGCCGCTTTGTTTACCAACTGTTA | AAACTTTCCTATTATACATATAATACTAACAGTTGGTAAACAAAGCGGCCG |
| 149 | 410 | GGAGCTTGCAGTGAGCTGA | P | CATGAGGAACTGTTTTCTTTTCTTTTT | | TTTTTTGAXACGGXGTCTCCCTCTGTC | ATCGSCCACTGCACTCCAGCCTGGGCGACAGAGGGAGACTCCGTCTCAAAA |
| 150 | 411 | AGAGATTAGTTGCTGGGCTTTG | P | GCTTGCAGACTTGTCCAGC | | CCACAAATTCCAAATAACAGAACCA | GTTGCAGGATATATTCCTTTGTTGGGTGGTTCTGTTATTTGGAATTTGTGG |
| 151 | 412 | TGAAGGAAAAAAAAAAAAAAGGC | | AAGCATATGGTCTGTCCTGGAG | P | TGACACTCTACCCAACAGCAAAAAA | TGACACTCTACCCAACAGCAAAAAAACCTTTCTTCTCAAGTATACGTGGAA |
| 152 | 413 | TGTGGATGTACCACATTTTATTGATC | | GTATATGACTCAAAGAAAGTCAGTTATTCTACG | P | GGGCACCTAGGCTGACTCCXTGTCTTT | GCACCTAGGCTGACTCCATGTCTTTGCTATTGTAATAGTGCTGCGATGAAC |
| 153 | 415 | TTTTGCACATTGAGTGCTTAGG | | GATTAGAAACCACCATGTTTACAGGA | P | AAGCCCTXAATCCAGAGAXATGTTTAC | GCCCTAAATCCAGAGATATGTTTACCACTTCCTGGCCCTGCCTTCYTAATA |
| 154 | 416 | ATAGACCTAAAGCCCTAAATCCAGAG | P | GTAAAACATTCCTCCAAGAACAGGT | | GGACCTATCCAGAAGGAGATTATTA | TTTACYACTTCCTGGCCCTGCCTTCCTAATAATCTCCTTCTGGATAGGTCC |
| 155 | 417 | AATATTTCCAGGAAGCTGCATTC | | CTTATCATATTTTTCTCTTTACCATTCTCTTAC | P | GGTAAGGGGAGCTACTGGTCATACA | GGTAAGGGGAGCTACTGGTCATACAGCAGCATGGAGTGAGTGAAGTGAGAG |
| 156 | 418 | TCCTCCAGGACAACAAGGATT | P | CATATAGGAGTTTATCTAAGGGAAATCACA | | TATGCCCTACAACTGCTATAACGCT | GTATTTGCATGCATGCAAAGAGTGGCAGCGTTATAGCAGTTGTAGGGCATA |
| 157 | 419 | ATCATGGCCTGATTGGCA | P | CAGAGCCATCAGTTCTCCG | | GGGGAAGCAGAGGGAAGACAGTGGC | GATCTTCCCCCAGGCTCTTGGTGCACGCCACTGTCTTCCCTCTGCTTCCCC |
| 158 | 420 | AAGAGAACAGGCTCCTTTTCAAA | | GTATTTTTTGTAGAGTGGAGGTTTTGC | P | AGGTCTGTGATGGGGTAGAAAGCAA | AGGTCTGTGATGGGGTAGAAAGCAAGAGTTCAGCCTGGCCAACATGGCAAA |
| 159 | 421 | GAAGGCTGAATGATATTCCATTGT | P | AGAGAGACTGCGGGACCAT | | GTGGTAGTTCTTTCTTTAXTTTTTTGA | TTTATGGAAAACAGTATGGACGTTCCTCAAAAAATTAAAGAAAGAACTACC |
| 160 | 422 | CAGCCCAAAACATTCAAGGA | | ATTTCGATGACCACTTACCCTTACA | P | TTCAXATCATTATTATTTTTTTTATAG | CAAATCATTATTATTTTTTTTATAGCTCACAGTGGCTGTCTGTGCTTTTGT |
| 161 | 423 | TGCCCTCTTCCTGTAACACC | P | CTGACTCCTTTTGAGTATCAGGGA | | CAGGGAACAAGCCAGRCTCTGTAGA | GTGAGAACTTCTTGTGCATTAACACGTCTACAGAGYCTGGCTTGTTCCCTG |
| 162 | 424 | TGCATATAGCAGATCCTGAGGC | P | AGATGATATTTGGGTGAGGACACA | | GGACACAAATCAXAACCAXATTATTCA | GTCTTCTAAATAATACATATTGTCACTGAATAATATGGTTATGATTTGTGT |
| 163 | 425 | GTTATGTCATGTGCTGTAAAGTTAGGTCT | | ACTTCAAAAATTCACATAGCACAATTG | P | TTAAAAATXAAAAATTTAGATTAAAAG | AAAAATAAAAAATTTAGATTAAAAGCTAAATTTAAGAAAGTTACTTTTGAA |
| 164 | 426 | TAGTTCAAGACCAGCCTGACG | P | GTTTCAAGCAATTCTCCTGCC | | CCCAAATAGCTGGGATTACAGGAAT | ACAAAATTAGCCGGGCGTGGTGGCGCATTCCTGTAATCCCAGCTATTTGGG |
| 165 | 427 | GCAAAGTATCCCAGACATGTAAACA | P | TCCTGCTATTCTTCAGCTAATTTGTT | | TGATAATTTAAAACAATAACAAGAG | TTTTCAACAGTACTAAAAGAAAACAGCTCTTGTTATTGTTTTAAATTATCA |
| 166 | 428 | TGTAAATCAATKTATTTTCAGTCCAGG | P | TTTACATTAGTTGCTTTCCTCAGGTG | | CTCAGGTGCACACATCATTCTCTCC | CTGCTCAACTACCATTATCCAGCAACGGAGAGAATGATGTGTGCACCTGAG |
| 167 | 429 | TGTTCTAGTTAGAAGAATTTACACTAGGAAAAA | | CCTCAGGTGCACACATCATTC | P | AATGGTAAGAATAGTGTAAATCAAT | AATGGTAAGAATAGTGTAAATCAATGTATTTTCAGTCCAGGGAAGGCTGCT |
| 168 | 430 | CTCTGATATTTACACTGACGATTTGCT | | TCCTGAGRCCTCCCCAGC | P | ATACAAGXTTAAAAGAGAAATCGTTGA | ACAAGATTAAAAGAGAAATCGTTGAGAATACAATTTCTTTTTTTTTTAATA |
| 169 | 431 | CAAAACACTTCTATACCTAATTCCCTTTT | | TKACCTTGATTTATACATGCTACGATC | P | TCTCCATGAAAAGATTXACTGTTAAAC | TCCATGAAAAGATTAACTGTTAAACGCCCTTTCTGCATCTGATGATCGTAG |
| 170 | 432 | GGGGATCTTGGGACGCTG | P | AATTGTTGGCTTGAAAGGTAATTCTAT | | ATTCTATTTTAAAYTCTTTGTGAAA | AGCCACTGTTGAAAGCTGTTTGGAAGTTTCACAAAGARTTTAAAATAGAAT |
| 171 | 433 | TATTATTAGGCCATTCTTGCATTGC | | CACCATGCAGATGCCGTC | P | AGGAAAAGAGATTTAXTTGGCTCACAG | GAAAAGAGATTTAATTGGCTCACAGGTCTGCAGGCTGTACAGGAAGCATGG |
| 172 | 434 | GGTACCGGGGATCTTGGG | P | TCTTTGTGAAAYTTCCAAACAGCT | | GGCTXAACTAATTTACATTCACACCAA | GGAGAAAAGGGAACATTAATACATAGTTGGTGTGAATGTAAATTAGTTCAG |
| 173 | 435 | TGGAGGTTTTGTTCCCAAAC | P | TAAAATGCGCTGGAAGCTCTC | | CTCAGCAGTAGAATCAAACAAGTAG | TCTTGGAGGCTCTGAAATTCTTTGTCCTACTTGTTTGATTCTACTGCTGAG |
| 174 | 436 | GAAACTGCCCCCATGAGC | | GTGTTCCCACCCAAATCTCA | P | CAATCACYTCCCACCAXGTCCCTCCCT | ATCACYTCCCACCAGGTCCCTCCCTCGGCACATGCGGATTACARTTCGAGC |
| 175 | 437 | GGCTTGCATTCCTAGTAAAATTGA | P | TTAGCTTTCTGAAAACTCATTATGTTGA | | ATTATGTTGAATATGGCATTTGGGA | GAGCCTGTATCCCTTACAGTAGAAACTCCCAAATGCCATATTCAACATAAT |
| 176 | 438 | TATATCAGTGGGCTCCTTCCTTG | | CTTTATAGCAGTATGAAAATGGAATAATACACT | P | CCTTTAAAACTACTGAAGTCTGAGC | CCTTTAAAACTACTGAAGTCTGAGCCTGACACCAGAGATTCTGATTTGCTT |
| 177 | 439 | CATGTGATAGAGTTATGGCTAGTGAATG | P | TTTTAGAATCTTTTCCATTTATCCAGTG | | TATCCAGTGAATGGGGAAAAAGAGA | AAAATCTTTCCACAAAATTCTTTGCACTCTCTTTTTCCCCATTCACTGGATA |
| 178 | 440 | TGATGAAAAAAGGCACATGTCA | P | GCCTCAAGTTTCAGGGCC | | TCTTTGCATGGGCTGTGGGAGAGGA | ATATGGCCATTGAATACCTTGCAAAGTCCTCTCCCACAGCCCATGCAAAGA |
| 179 | 441 | GCTAGACATTTTCAATAGGCACCTC | P | TGTAGCCCAAGGTGGTCAGA | | AAATATAXATTTTATTTGACATCTCCC | AAAAAAGTTTCCAAAATTTAAAAATGGGGAGATGTCAAATAAAATCTATAT |
| 180 | 443 | CAACCATTTTTCTGATAATTCTGTGA | P | AGGATGTCACCATTTTTGTGGT | | TTTTTTGCAATAATCCATTAGAAAG | GTTTTATCTTTTCTTAAAAATGTGTGCTTTCTAATGGATTATTGCAAAAAA |
| 181 | 444 | TRCTCCTTGATCCGTGGAGT | P | TGCACCTAGTTACCCAAGAGCT | | AAGATGTWCAAGATCAATGTTTTCA | CAGAATGGATGTTGTATTAGCAGACGTGAAAACATTGATCTTGWACATCTT |
| 182 | 445 | TTTGCTTCCCCTTCTGCC | P | CAATTTACTGTATTAGCCTGTTCTCACA | | GAGTGGGCAATTTACAAAGGAAAGA | CTATGGAACTGTGAGTCTATTAAATATCTTTCCTTTGTAAATTGCCCACTC |
| 183 | 446 | AGAAGTCTTTTACATGGAAGAAGAAAAAA | P | CRAAGACTAACAAAGGTGGTCTAAGG | | GTCTAAGGAAAGGAGAGGTTTCAATAGACGGTACACTCGGTTGTTCCCTTAGAC | |
| 184 | 447 | AGGAAAGTCTTTGACTCCATCCTC | | AACCCCAGCTATTCTTATTAGCACA | P | CTCATACTCAGACCTAXTTCCTTCTAA | CATACTCAGACCTAATTCCTTCTAACAAAGGTTCTTTGGAAGGTATGTGCT |
| 185 | 449 | CCCACCTCTAGCAATGCAG | | CAAATCAAAACCCCAATGAGATAC | P | TTACAATTCAACATGAGATTTGGGC | TTACAATTCAACATGAGATTTGGGCGGGGACAAATACCCAAACTATATGAA |
| 186 | 450 | CTGGGGCCAACTGCATTT | | AAGCTGGTGGTAGTAGAAATACATGG | P | CCACCTGGATTCCACAAGACACCCT | CCACCTGGATTCCACAAGACACCCTGGCATCTTTATAATAAAATCCATGTA |
| 187 | 451 | AAACAAGAAGACAAATGGAGGTTG | | GTTTCTGTGGAGAGGACCGAC | P | AACCAGTTAGAGTTCCATTTTGTGC | AACCAGTTAGAGTTCCATTTTGTGCCAGGACAGTTCTGCCAAAAAGAACTT |
| 188 | 452 | CAGAATTGCATTGGCTATTTGG | | TCCCCATGTTCGTGGATTAG | P | AATXTCTTTTGTATTCGGATAGTGA | AATATCTTTTGTATTCGGATAGTGACTTAATTCTGTAGCTCTCTTTTGGTA |
| 189 | 453 | GTTCAACTACTTCCCACCGG | P | TTTCAGGTTTCAATGTGTACTTTTAACA | | TATTTATAGATTAXATGTATTTAATTTATGTAATAAAATACATTTAATCTATAAA | |
| 190 | 454 | TAGAAACTGGAAAAAGAGGGAGC | | GATACAGASAAGATTGCAGTGTGG | P | GATGCAGTCAAGGCAAGGAAGAGGG | GATGCAGTCAAGGCAAGGAAGAGGGGGAAATACCCTTCTTCTTGCTTTCCA |
| 191 | 455 | TCATGGCTGGAAATGAAAGTATC | P | CTGGAATGGGAGAATAGTGTGTTT | | CAGTCACAAAGCAGAAGACCAACTC | TGAAGTTCCTGAAACATTACTTTACCGAGTTGGTCTTCTGCTTTGTGACTG |
| 192 | 456 | AAACCCCGCCGAAGGTAC | | TTATTCATTTTTTTCCCCAGCAC | P | GAGGATCTGCTGCACCAGGCAAATT | GAGGATCTGCTGCACCAGGCAAATTCTGTGCAAAATGCAAATTTCTGTGCT |
| 193 | 457 | AAGTGGGAGGATCACTTGAGC | | CTTCTTTGTCTTTTGTGAGACAGTGT | P | GGXTXCAGTGAGCTGTGATAGCACCAC | CTGCAGTGAGCTGTGATAGCACCACAGAACTGCAGCCTGGGTAGCAGAGTG |
| 194 | 458 | ATGGTGAAACCCATCTCTACTAAAAATAC | | CTAGGTTCAAGCGATTCTCCTG | P | GGCGTGGTGGTGCACTCCTGTAATC | GGCGTGGTGGTGCACTCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGG |
| 195 | 459 | CTGCCTTCCTCTTTGCCTTC | | TTATAAAGAACAGAGGTTTAATTGGCTC | P | GTAAGTTTTCTGAGTGCCCCCCTCC | GTAAGTTTTCTGAGTGCCCCCCTCCCACCTTGATCATGTTTCCTATACAGC |
| 196 | 460 | CGTAGAGTGAAAAGGAGTGGGA | P | CTGGCTTGGGACGAAATTTT | | TTGAATGAATTTTTTTTTAGCATAAA | TGAAAGTATAAAACCCTTAAAAGACCTTTATGCTAAAAAAAATTCATTCAA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 197 | 461 | AGCTGCCTTCTTGCTGTGTC | P | GAACTGATAGGATTAGTGTCTTTATAAGAAGAGA | | AGAGGGCTGGCACTTTCTTTCTGTG | CACAAGGCTTTTCCTGAGTTCCTGCGCACAGAAAGAAAGTGCCAGCCCTCT |
| 198 | 462 | CTGGGGGCTTTGTTTTGTTT | P | AGTGACCATATCACCCATACAATCTATAG | | AGTTAATGCAXTTCCCATCAAATTA | TTTTAATTTTGTGRAAATAACGTTGGTAATTTGATGGGAATTGCATTAACT |
| 199 | 463 | AGCTGGTATCCTATGGGCTTTT | | CCCAAGACAGCAGCCATG | P | CCAGCAGAACTGAGAAGAGGAAGGT | CCAGCAGAACTGAGAAGAGGAAGGTGGGGGAGCCCAGCTTCTCGGTGACTG |
| 200 | 464 | GTTGAGTTCAATTATTTTTCTTTTCCAC | | TGGTAAATCAGAGACTGTAGTTATCCATC | P | AATTGGGTCTAATTTGATAAACTCC | AATTGGGTCTAATTTGATAAACTCCGTTTCCAGCGGTTAAAATATAGATGG |
| 201 | 465 | AGCTTGGGTTCAAGAGGGAG | P | TGGCCTGAAGCCCACGTC | | TCGXAATGCGCTTCAGAGGCTTTTCCT | TCCAGCAGGCGTAAGTAGTGGCTGCCAGGAAAAGCCTCTGAAGCGCATTCC |
| 202 | 466 | TCCTGGGTTCAAGTGATCCTC | P | CAACATATGGAGATCCTATCTCTACAAAA | | AAAAAAACCCAAAXTTAGCCAGCCA | GCTGGGACTACAGGCTCGAACCACCGTGGCTGGCTAATTTTGGGTTTTTTT |
| 203 | 468 | ATAGAAATGATTAGACATCAGGAAGAATTC | P | AGCTAATTTTACACCTAGATAGCTGGAGA | | GAGATGTGGTTAATAAGAAGAAACA | TTTTCCTTCAAATGTTATTCAAAATGTGTTTCTTCTTATTAACCACATCTC |
| 204 | 469 | CACTTTACTTAGTATTTCAAAAACTTCTGCA | | GTTTATACTGATGCCATTATATTCCTGATC | P | ATTGXGAAGAATGAATCTCTCACTAGG | TGTGAAGAATGAATCTCTCACTAGGAAGTTGCATTAGAGGATCAGGAATAT |
| 205 | 470 | TTTTTTTGGTCATATAAAGCTAATGGG | P | GTACTTTTAAATGAAAGGCTGTGGACT | | TGTGGACTCCCATGAACCTAGAATG | ATTTTTTCAATCTCAGGATCACACAGCATTCTAGGTTCATGGGAGTCCACA |
| 206 | 471 | CAGCCTCCAAAAAGACAAAGTC | P | TCTGTAGCCAGCAAGGACTGTAT | | ATTAAGAAAAAAAAAAAAAAGATCAG | AAAATGCTTACCCAAGTCAATGAGCACTGATCTTTTTTTTTTTTTCTTAAT |
| 207 | 472 | AAAAAAATAGCTGGCATCCAA | | GCCAACCTCGTCTGAGCTC | P | GCTGACCCAGCCCCCTTTGTCTCCC | GCTGACCCAGCCCCCTTTGTCTCCCGCCTGGGTCCCAGAGGCAGCAGAGCT |
| 208 | 473 | ATTTCTGTCCTATCAGAATGTCCTTTT | P | GATTGTAAAATGCACCAATCAGC | | TAAAACGCACCAATCAGCAGAATCC | ATCTTCCCTGTGACTGGCTACTTTTGGGATTCTGCTGATTGGTGCGTTTTA |
| 209 | 474 | TTAGTGGACTGAAGTTATAGGTGCTAAGA | | TTCTAAAATGCTTCACATCCCC | P | CATTXACTTTTTCTGTAACTTAGGAGAGTAGGTCACCCATCAGCAAAAGGTAA | TTTACTTTTTCTGTAACTTAGGAGAGTAGGTCACCCATCAGCAAAAGGTAA |
| 210 | 475 | GAAGGCAGAGTAGGTTTTTTTAATTCA | | TATGGGCCTGTATTTCTGATATTTCA | P | TAATTATTTTCCTTGGCAGGGATTT | TAATTATTTTCCTTGGCAGGGATTTGAAACATTATTTGGCAACTGAAATAT |
| 211 | 477 | GACAAGTTTTGGCTGTTGATCTTC | P | CCAAATCTTCCAAAGTAGGCAA | | CAAAGATACAAATTTTCAGACATTG | AAATCAATCTAAGTCTGGCATTTACGCAATGTCTGAAAATTTGTATCTTTG |
| 212 | 478 | TTAGTTCACAGTACTCGATAACCCTTG | P | GCCCTTCCACTCTACACACAC | | CACCGTCGGTAGCTTCCTCATGCCT | GCACTCGGTTGAATACTAATTAATACAGGCATGAGGAAGCTACCGACGGTG |
| 213 | 479 | TCCACAGCAAATAATGCATGAA | | GTTTCATAACTGATTTCTTTTTCCAGTG | P | CCTTGAAACTACTGAACTCATTAGT | CCTTGAAACTACTGAACTCATTAGTAGCCGGAGCAATAGACTGAGTGCAAA |
| 214 | 481 | TTTTTTTTTTTAAAGACAAGTCTCGC | P | ATTGCTTGAACCCAGGAGG | | GCGGAGGTTGCAGTGAXCTAAGATCAC | TGTCCGCCAGGCTGGAGTGCGGTGGCGTGATCTTAGCTCACTGCAACCTCC |
| 215 | 482 | TTTACAACTCAGAAAGGGAAACAAG | | CTATAATGCCCCACCTCTGTTCT | P | TCCCCTCCTCTGGTTTTTTGTTTTTT | TCCCCTCCTCTGGTTTTTTGTTTTTTAACTGAGTCATG |
| 216 | 483 | CTAACCAACAGCCAATAAGAGAAAAT | | TGCATAAAGGTGAACTCTTCTTGC | P | AACATTTGGAATTTTCTTACCTTTA | AACATTTGGAATTTTCTTACCTTTACGCAGACTTTTCACTGCTCAGAGCAA |
| 217 | 484 | AAAAATAGCCTTGACTGACAAACTATGTATA | P | CAGGCTCTTGAGACCTCTTTCTC | | CTTTCTCXAAGGAACTCTGXTCTGGCT | TGGGATTGGAATGCAGCAAGCCCAGCAGCCAGATCAGAGTTCCTTGGAGAA |
| 218 | 486 | TTATCTTAGGTTTCGGAGAGCCA | P | CATAATGAGTTCTCAATAAATGTCAGGTC | | GGCTCCCTCTTCTCTAAAATCCCAA | CAGGCCTTGAAAGCCTTCATCATGGGTTGGGATTTTAGAGAAGAGGGAGCC |
| 219 | 487 | AACCAAGTATGGAAGCCTTCTCC | | CACCCTAGAGGTTAACAGGACCC | P | AGATGTXTCAGGGAGCTTGGAGAAAAG | ATGTCTCAGGGAGCTTGGAGAAAAGGTGACAGCCCTGCGGATGAAAGGGTC |
| 220 | 488 | CAACCTCCACTTCCCAGGT | | CTACTAAAAATACAGAAATTAGCCAGGC | P | TTCAAGXAATTCTCCTGCCTCAGCCTC | CAAGCAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGAATTACAGGCCCAT |
| 221 | 489 | GGTTTTCAGAGGCATTCAAGC | P | TGCTTCAACAGACCTCAGTATTTCT | | CAAATTAAATTTAATCACAGGTATT | GTCTTTTGTTTTCTGACCAATCTAAAAATACCTGTGATTAAATTTAATTTG |
| 222 | 490 | ACAGCCTCCAGGAGACAGAC | | CTTAATCACAGCCCTTTGGTATGT | P | CATTCTTTGGTAAGTCCXAGTGTGTCT | TTCTTTGGTAAGTCCTAGTGTGTCTAATGAGGTGTCACAGGCCTTGAAGAC |
| 223 | 491 | TTATATCTAGTATGGTAATTTTTGCAGGGT | | CTAATCTTTACTGTCAGTCTTAGGAAGGTAATTA | P | TCCAGGAAGCAAGCCACTTTAGCTA | TCCAGGAAGCAAGCCACTTTAGCTAGAACCCCTGCGGGTTGTCACACAAAG |
| 224 | 492 | CACTTTTATCTTCACAGCGCACT | P | AGTGTCATTTCATTTCCTTGTGTATG | | TTCXAGGGTTTCTGGGATTCTTTTGGA | CCAGGGTTTCTGGGATTCTTTTGGAGAAACTAAAAATACACTAATTTTATA |
| 225 | 493 | AAAATGATCAAGCCTTTCTTTCATG | P | GTTATACTACTACTTTTAGACCAAAGATCCAGC | | GACCACCAACTCAAAAAACACAAAT | ATTAAACAATGTCTGCTTTGTAAGAGATTTGTGTTTTTTGAGTTGGTGGTC |
| 226 | 494 | ATAAGATGAAGTGCAGATGCAATG | P | CTTTCAATTTTTCTCTTCTCTCTTGCTA | | TTTGTAAAACCACTGTTGCCATAGT | AGACCAAGTGGTTGTGGCACTTAGTCACTATGGCAACAGTGGTTTTACAAA |
| 227 | 495 | CATGGTATCAACCTCTATGTGCAT | P | CAAGTGCTGTAAAGGAAAAGCAG | | GGGAGGGGAAATAGCAAGTGTTATA | GGGCAGCAAGCTCATTGATTGCTTGGTATAACACTTGCTATTTCCCCTCCC |
| 228 | 497 | TTGCAGTGAGCCGAGATG | P | CATCATACCTGGTTGGGAGATG | | ATGGGGAAXCAGATGCAAAATGATGAA | AAAAAAAAAAGAACTATTTCTCCTCATTCATCATTTTGCATCTGATTCCCC |
| 229 | 498 | GACAACAATTTGCCATGCATT | P | GGCATTGGCTTAATGACCATT | | AGTGAAAAATATGAGAGGCAAAAAG | TTACATGCATTACAAAAATAGCAATGCTTTTTGCCTCTCATATTTTTCACT |
| 230 | 500 | TATGTACCTAAGTTAAAACTGAAGGGTCC | P | CATCATGCTCTGGGGTCACTA | | TACAGGACTACCAAXTTCACATCTG | CTGTTTACAAATGACACATTTCCATGCAGATGTGAATTTGGTAGTCCTGTA |
| 231 | 501 | TTTAAGTTCTGGGATACATGTGCTG | | AAACCTAGATGATGGGTTGATGG | P | TGCAGGTTTGTTACATAGGTATACA | TGCAGGTTTGTTACATAGGTATACACGTGCCATGGTGGTTTGCTGCACCCA |
| 232 | 502 | CCTAAATACCATTTGAATTGATAAAGATGTA | | AGTACTAGTGAGTATTTGATTACTAGGTTACACTA | P | CTCAACTCAACTCTGCTTATATGTA | CTCAACTCAACTCTGCTTATATGTAATAGATCCATATCCCTTATGTAGTGT |
| 233 | 503 | TAAGATGCAGGTGAAGTGGCTTA | P | AGTTCAGTTCTACTAAAAATCTGGGCA | | GGCAGGCAGTCTGAGACAAACTCCC | AGGAAGTAGTTCAATTTGTATTTGTGGGGAGTTTGTCTCAGACTGCCTGCC |
| 234 | 504 | TGAAGGCAGTTTAGTCACCAAATTA | P | GGGGAGTAGAAATTGAGAATAGGG | | AGGGGATXGCTAATTTTCTXCAATTCG | ACTTGGTTTCAGAGCTCTTGAGTTTCCGAATTGCAGAAAATTAGCAATCCC |
| 235 | 505 | GCAACTTAATCTCCATTGCAGG | | TCTAGATATTTATGCCAATCCCATCA | P | TTTTATAGCATAGTAXTTTGGAACATT | TTATAGCATAGTAATTTGGAACATTGTGTGGCATTTTTATAACAAAAAAAC |
| 236 | 506 | TGTAGGGAAGTATGTTATGCAGAGC | P | AGTCTCTTGTGACAAAAATGTACCAG | | GACCCAGAAACTGATATXAATGCTTCA | CCCAGAAACTGATATGAATGCTTCAAATAAATTCTGCAGAAGCAAAGCTGG |
| 237 | 507 | TAAGATGTCTCTTAATCCAGTTTTCCC | P | AGGACAGAGGGAAGTTGGGA | | GAGGAGGGTCCAGGAAAGAAGGGAA | GTAATCTCTACCAGATAATCCAGCCGTTCCCTTCTTTCCTGGACCCTCCTC |
| 238 | 508 | GGCCTTTCCCACACCAGC | | CTTCCGAACTTCCCTCTGTCA | P | GAAGGGTAGCCAGGCAGTAGAATTT | GAAGGGTAGCCAGGCAGTAGAATTTCATTCAACCCTAGGGTTCCCACCTGA |
| 239 | 509 | GTCAGGCCCCCAGATGAG | | CTGGTCCAGGTAATAACCCAAAC | P | GGCTGCGGCATCGATTCTGACCACA | GGCTGCGGCATCGATTCTGACCACACATTCTGGAAAAATTATCATCCTACA |
| 240 | 510 | CCAGCAGCTCAAAAACACTTG | P | ACCCCTTTTTCTTAGGCATGTTT | | TGAAAATAAAATAATAAGAAATATA | AACATAAATAATAATGTACTTAATAGTATATTTCTTATTATTTTATTTTCA |
| 241 | 511 | CCACTGACGTTATTCAAATGTACAC | | TCTTTCATAACAAAAGAAGAACAGC | P | ACAGATGTGAAAAATAGCATAAGCA | ACAGATGTGAAAAATAGCATAAGCAAACACAACCTTAACAAGGCTGTTCTT |
| 242 | 512 | TGCCTCATTATTATGGGGGAA | | CATGTCTGGACAAACCCTCCT | P | AGGGCACTTGTGTGGTGGAATAGGC | AGGGCACTTGTGTGGTGGAATAGGCGGGATGGGGGTGGTGCATTTTATCCA |
| 243 | 513 | ACATCAAATTGTACTGCAATAATATGTACAA | P | TGCATGTTAGAATTTTCTGGGC | | GXACTGTTGAAAACTCCCCXTGCCCCA | TCCACAGAAGTTTTCATTTAATTGTCTGGGGCATGGGGAGTTTTCAACAGT |
| 244 | 515 | TTTCATTCTCAGTAGAGCTTCAAGG | P | TAATGACCACTGGCGCTG | | CCTGCTGCTCTCTGAACTCCTCTCT | TTCCCAGAGAAGGGGCACAGTTCCACAGAGAGGAGTTCAGAGAGCAGCAGG |
| 245 | 516 | TTTATAGGGTTTGGTTTTATTGGGA | P | GAAGCTGCTGACTGCCTGA | | TGATCTCTGTGAAACTTAGGTGTAA | TTTGAGCTGTATAAAACTGTAAACACTTACACCTAAGTTTCACAGAGATCA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 246 | 517 | TACACAGACGCTCTTAAGTATCTGACA | | AAAGATGTCAAGGCTTCAGAAGG | P | GTAGTGACCAGCACTCAAAGATAGC | GTAGTGACCAGCACTCAAAGATAGCGCATATGAGCGGCTCAGTCAATCACT |
| 247 | 518 | AAGCAGCGACCCGACCCG | | GAATGTGTCACCTGCCATGAC | P | TGGGGTCCCTGGGGCAAGCGAATGG | TGGGGTCCCTGGGGCAAGCGAATGGCCCTTTGCCTGGAGAACCTGGGCCAG |
| 248 | 519 | GCTAATGCAGTGAGTTTAAGTGTTTAATT | P | CACCAGCAGTTACTAATTTTTTCTAAATTAA | | AACACTTAAACTCACCGCATTAGCA | ATTAGTAACTGCTGGTTGCCTCATAGTGCTAATGCGGTGAGTTTAAGTGTT |
| 249 | 520 | AGAATGGTGTGAACCCGG | P | CCAGAAAGAACTATTTCAGGCTTAGTT | | TTAGTTTTTTCTTTTTCTTTTTTTT | CAACAGAGTGAGACTCCGTTTCAAAAAAAAAAAAGAAAAAGAAAAAACTAA |
| 250 | 523 | TTCAGGCTGCACCCCTTC | | CTGTGGACTCCCTGACTTCC | P | ACGAACTCGGATGCACCTCTGTGAG | ACGAACTCGGATGCACCTCTGTGAGAGGACTGCTCAGTTCACCGGGGTGGG |
| 251 | 527 | TTAAGCAGCTTGCCCAAGG | | CATGGCGTCGTAGTTGCAG | P | CTAGTAAGCAAGGAACTGAAAATGA | CTAGTAAGCAAGGAACTGAAAATGACGCTGGCCTGTCTAACGTGACAGTTC |
| 252 | 528 | ATCAGGAGCACTTGAGCCC | | GACAAGGCGAGACTCTTGTCTC | P | ACCACATCCTAACATCGTAACAAAA | ACCACATCCTAACATCGTAACAAAAGGAGACCCCCATCTCTACAAAACAAA |
| 253 | 529 | CTCCACATTACCAAGAGGATAGGTC | | GTAAAATGCTCAGCTCAGATGGA | P | AAAGCACCAATAACAACAGTAGCAG | AAAGCACCAATAACAACAGTAGCAGCTCATATTCACTAACTGCTCAACATG |
| 254 | 530 | AACATTCTGACTGGCGCTGT | P | CTCATACATCTGTCAGTAATAAAGCCAA | | GATAAGTAACTGAGACTGAAACGCC | CTGTGGTCAGGGAAATGGAATACAGCGGCGTTTCAGTCTCAGTTACTTATC |
| 255 | 531 | TGCTGGGATTACAGGCATG | P | AACCTTTGGCTAAAAGGGTCTG | | CTGATTACCCAAAGAGATTAGAAAC | GCCACCATGCCCAGCCGCCAAGAGGAGTTTCTAATCTCTTTGGGTAATCAG |
| 256 | 533 | TGCTCACCATTTTTAAACATTTATTTG | | GAGGCAGGAGAATCGCTTG | P | TTCTTTTTGAGGTAGAGTCTTGCTC | TTCTTTTTGAGGTAGAGTCTTGCTCCGTCGCCCAGGCTGAAGTGTAGTGGC |
| 257 | 534 | TAGCTGGGATTACAGGCGC | | GATCACTTGAGGCCAGGAATT | P | AATTTTTGTATTTTTAGTAGAGACG | AATTTTTGTATTTTTAGTAGAGACGGGGTTTGTGCCATGTTGGCCAGACTGG |
| 258 | 535 | TGAAAACCAAAGCATTGATAGGG | | GCCAAAAAGGCAACAGGG | P | TGCATTGAGTTGTTGGCAGAATTTC | TGCATTGAGTTGTTGGCAGAATTTCGTTCCATGGTGCTGTAGGATTGAGGT |
| 259 | 539 | AGTTTTCCTTTTCTTTTTCCCATG | P | GTAGTAAATGGCATAGAAGACAGGGA | | GACAGGGAATAAACAAATAATCTGA | ATCAATGGTGTGAGCAAGGCCACTCCTCAGATTATTTGTTTATTCCCTGTC |
| 260 | 543 | CACACACACACCCATACATAAAAAA | P | ACGTTTAGATATTTTTCTTTATTGAAGGATG | | TTCTTTTTATGGCTTGTTTTATATC | TAAACATTATAGAAAAAACATTGCAAGATATAAAACAAGCCATAAAAAGAA |
| 261 | 544 | CTGATCTGATTTCACAGTAAGCTNTTTAC | | TCCCAAAGTGCTGGGATTAC | P | TTGGAATACTTTTAGATATACAGAA | TTGGAATACTTTTAGATATACAGAAGAATTATAAAGATAGTATAGGCCAGG |
| 262 | 545 | GTTTAGCCAAAGATTTGAAGCCA | P | CACTCAGATTGTAAAATTTGTAATGCA | | TAGAAAATCCTGCTTAGTTTAGGCA | CAATCCTCTAACGAGTACTGTAGTGATGCCTAAACTAAGCAGGATTTTCTA |
| 263 | 546 | GTACATAAACAGTCCTGCCTGCA | P | AGTATGTTCACTTGATTTACACTCAAGTATTTAG | | ACTCAAGTATTTAGACCTTTTGTAC | TTGGACCCCAGAATAAGAATATTCACGTACAAAAGGTCTAAATACTTGAGT |
| 264 | 547 | CCTTAAAAGTTTTCTTGTTCACGTAATTAT | | CTTCATTTAAAAAAAAAAGTAGAGGACTG | P | ATTAGTTTGTTAATCGGTGTTTTGG | ATTAGTTTGTTAATCGGTGTTTTGGCTGGACCATATGGCCTTTTTTTCTAA |
| 265 | 548 | GGAGAATAGGCTCTCATATGTTAGGTAAG | P | ATGGCTTGCTTCTTCATTTGATT | | TGATTCCTTTCTCTGCTCCATGTCA | AATCAGGAAAGATTTCTTTAATAAACTGACATGGAGCAGAGAAAGGAATCA |
| 266 | 549 | AAGGACCGGACATTTTCACTTC | | ATATACATCCAGATGGCCTGAAGTAA | P | GTGGAATGTCATCAGTXAAGGCAGGAA | GGAATGTCATCAGTTAAGGCAGGAAAAGGCCATTTAAATTTCACTTCTTTT |
| 267 | 550 | CATGGTTTTTTTAAATGGACTATCCA | | AGAGACCACAAGAATAACTCTTYGAATATAA | P | TTATCTTTATTATTCATTCXTGTTTAT | ATCTTTATTATTCATTCATGTTTATGTATTATTTAATATTAATATTATTAT |
| 268 | 551 | TAGCTTTCAAAAATCTACCCCCC | P | CAAAAGTGGAAAAAACAGATTGACC | | ACCCCAAATGCTATGCTTTTCTTCA | CCCCTCTGCTGGGACATATGATATAGTGAAGAAAAGCATAGCATTTGGGGT |
| 269 | 553 | AAGGAATGTATCCCTCACTCCAC | P | AGGCATTGCTTAGTTACTGGTTGT | | TGTCTCCGCATATTCAGAAAAYAAT | CATGGAAATAAAACCAATCTCAGATAATTRTTTTCTGAATATGCGGAGACA |
| 270 | 554 | GCCAAATCTGTATTCCCAAGTATTT | P | AGAGAGAGAGAGAGAGACTGGTAATAAATAATG | | ACTGGTAATAAATAATGGXTTAGCAGG | AAATGTTCCTTTCTGTTAACTGCAGGCCTGCTAAGCCATTATTTATTACCA |
| 271 | 555 | TTTTAAACATCTGCACGTTTCTGA | P | CATTTTGTAACTCCCACATCTGG | | TGTTGCCTGCCTCTTTTGCTTCTAC | CCAAAAATGTATTTAAATCTCAACTCGTAGAAGCAAAAGAGGCAGGCAACA |
| 272 | 556 | AAGGAGTCCAAAAACCTTTGACC | | GATCTTGCAGCCTTTTTGCA | P | ACTGAXAGTTGTAAGAACTGACCTTTG | TGAAAGTTGTAAGAACTGACCTTTGGCCTAGGATTATGACTCTCATGTAAG |
| 273 | 557 | AATAGCTGACTTCTCTTCCATTTCTG | P | AATGGTACAGCACTTTAGTCATACCAA | | CATACCAACCCTCCAGAAAACAAAA | TGGTATTTTTTTCCAGATTTTATAAGTTTTGTTTTCTGGAGGGTTGGTATG |
| 274 | 558 | TTAGGGACTTAGCTGTCTCTCCCT | P | GATGTTCATAGACATGCAGACAGATT | | TGATGGCAXTGATATTCAGACACATTA | TCRGATTTTTCCAGCAGATATATCTGTAATGTGTCTGAATATCATTGCCAT |
| 275 | 559 | AATCTCTCAATCTCTCAGCCTTTCT | P | CTAACACCGTGTGTGTGTGTGTG | | GTGTGTGTGTGTGTGTGTGTGTGTG | CTCTCTCTCTCTCTCTCTCTCWCACACACACACACACACACACACACAC |
| 276 | 560 | CTCCTTGTACTTCGAGACCTCAGA | P | TCAGATAAGTAGTACACAAACAATTAAAATAAGG | | ATTAAAATAAGGAATXCAATAAAGTAA | TGGAGGTCTTTTGTGATCACCCAGTCTTACTTTATTGCATTCCTTATTTTA |
| 277 | 561 | GGAGAATCTCTCCCTTCAGGAA | | GACCATAATGAATTAATCAAAATGGAGA | P | TCTCTTTTTAXAGGCTTTTACCTGATT | TCTTTTTAAAGGCTTTTACCTGATTAAGTCAGGCCTTCCTAAGATGATCTC |
| 278 | 562 | CAGCCTGTGTTCCCTGTCC | P | TGACCTTGTCATTTCTTCCATTCT | | ACCTAGTTTTTTTTTTTGTTTTTTT | TAAAAAAAAACAAAAAAAAAAMCCCAAAAAAAACAAAAAAAAAAACTAGGT |
| 279 | 563 | GAATTCTTAATTTACTTTGGCTATCACC | | TCCAAGAGTCCAGAAGGGG | P | ATTTTGTCATGTTXAAGATCCTCTA | ATTTTGTCATGTTTAAGATCCTCTAGTCCTGGATGTGTCTTATACCTCAGG |
| 280 | 565 | GTCATCCCAAGAAGAGATAAGGG | P | TTTATGTAGGGGTTATTTAGGATTTCATAA | | TTTCATAAACAGATGTAAAXGATTCTT | GAATCAGAGAAGAGGAGCCTTCAGACAAGAATCTTTTACATCTGTTTATGA |
| 281 | 566 | TTACTCTGTTGTCTTCTCATTGTTCAAT | P | CAGGAGCTGCCATTTCAGAC | | CAATAACCACGTCTTCAACTTTTCT | GCACTGTGCTAAGTACTGCGAGAAACAGAAAAGTTGAAGACGTGGTTATTG |
| 282 | 567 | AAGTTTACTATGTGAACTTGGGAAAATC | P | TCTGTGCTAAGCACTGGGCT | | CAAGAGTTTTTTTTATTGTTTCCAC | CATATCTTTTCTCTTGTATATTTCACGTGGAAACAATAAAAAAAACTCTTG |
| 283 | 568 | GGGGTCTTATTCTTAGCAGAGCA | | TGTTGTTTTTGTTAAGAATCTATCATCC | P | GGAAACATAGTAGGCACCCAAGTTA | GGAAACATAGTAGGCACCCAAGTTAGGATTTGATGATGCAGAATGGGATGA |
| 284 | 569 | TTTCCCAGGATGGAATTTTGT | | GACAACAGAAAGAGATGTGGCC | P | CTCCAGCCAGTTGTATAGAGAACAC | CTCCAGCCAGTTGTATAGAGAACACGTCAGACAAAACCTTTTCAGATGGAC |
| 285 | 570 | GGACTTGCATAGCAAAAATCAAC | | TGTCAGTTTTAGTCACTGATAATAACCCT | P | ATGACTAGGAXAACATTTTGTAATT | ATGACTAGGAAAACATTTTGTAATTCACTTGTGAATAAAGACTAATTTATA |
| 286 | 571 | AATTCCCCTCTCTAAGCCATAGTT | | GAATGAACCAGACTTTAGTGTTCAGAC | P | CTAAATGTGTGAGAAAAACAAGCAG | CTAAATGTGTGAGAAAAACAAGCAGCCCACACATAGTTCAGGGCCTGGTCT |
| 287 | 572 | GTTTGCTCTGGATCTTCTTTGG | P | TGAAGAAGTCTCCAAATTGTGAAATATAT | | ATATATTCCTTTGTGCCCAGTCTAA | GGTTTTCTACTAAATATTTTAAGTGATTAGACTGGGCACAAAGGAATATAT |
| 288 | 573 | TAATATTGATCTCTGGATTATTGACAGG | P | TGCAATGAAGATTTACTAGATGAAATGA | | GAAATGAGAGGGTGGGGCTAGAAAA | TTAAGTGAGATAACTTGCGTGGTCCGTTTTCTAGCCCCACCCTCTCATTTC |
| 289 | 574 | CACTTTAGAGATAAGGAATTTTACTATACGTTAGA | | TTCTAAAGAACATTGGGTACTAGATTCCT | P | GAAACCXTAATTATCTATACTAAGAAG | AACCTTAATTATCTATACTAAGAAGACCTGATGAAATTATATGTTAAAGCA |
| 290 | 575 | TTATTTTGTATAAGCTATAAAGCACCTAACTATCA | | TGATCTGCCCACCTCGGC | P | TACXTGTTGGXCGGGCATGGTGGCTCA | CATGTTGGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAG |
| 291 | 576 | CAGCACCATGCTTCCTGTAC | | ATAAAGAAATGCCTGAGACTGGG | P | CAGCCTGTAAAAXTGTGAGCCAATTAA | GCCTGTAAAATTGTGAGCCAATTAAGCCTCTTTTCTTTATAAATTACCCAG |
| 292 | 577 | TCAGCCTCTCTACTCTAGCCATACTC | P | CAAGAGTTATTCGTTGGTTTGTTTTC | | AGTCATAATAXAGTCCATXAACCTTTG | TCATAATAAAGTCCATTAACCTTTGCGTCCAGCTCTGCATGCCCAGTAGAG |
| 293 | 579 | TGCTCGGCTGTGACCTCT | P | CAGTTAGGACTCCATAGCAGGC | | GGCCTGCAGTGGCCCTGXTGATAACCT | CAAGCATTCTTCCATGCTCCTCCCCGAGGTTATCACCAGGGCCACTGCAGG |
| 294 | 580 | TTAAATGGCTTCCCCAATGAC | | GAAGAGTTCTACTACAATCGTATTGCTGT | P | CCAAATCAATAACAGTGCCCCCAGT | CCAAATCAATAACAGTGCCCCCAGTGAAACACAGCACCTTTGTTACTTAAA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 295 | 581 | GCATTGCAGAAACAAAGTTCAGT | P | TTAGGCCATTGCTYTTTTGATG | | TTGATGTTXCAGAAACAGTGGATTCAG | CTTTTAAATCCTACTGGGCAACCAGACTGAATCCACTGTTTCTGGAACATC |
| 296 | 582 | CATGCGAGTGGGACCATG | P | CTCTTCCTCCTCCTGGTGTCTT | | ACTCCCCACTTCACACTCCCATCTA | GACTGGAAGTGGGCCATCCAGACTAATAGATGGGAGTGTGAAGTGGGGAGT |
| 297 | 583 | TGTACAGCAGTGCCAGAGAAAA | P | CACATCAACCTGTATGATCTGCC | | TTGAGATAATCCTCCAAAACTACTT | TGTGTCTCAAAAACCTTCAATTAAAAAAGTAGTTTTGGAGGATTATCTCAA |
| 298 | 584 | CGCTACTTATTTATTTCTATCCCAAGC | P | CGCCCAGCAGCAGCTTCC | | TTTGCCCCTCCCAACTTCCASCCTG | CAGCAGCGGCGATCTGCGACTGCGCGCAGGSTGGAAGTTGGGAGGGGCAAA |
| 299 | 585 | CGAGAGAGTATATCAAGAAGGCAAAG | | TATGCTCAGAGTTTTGTGAGTCAATT | P | ATATTTACCCTGCAATGGAAAATTT | ATATTTACCCTGCAATGGAAAATTTCGTCAATTAGGCAAATTGAATTGACT |
| 300 | 586 | ATCACGAGGTCAGGAGTTTGAG | P | GATTACAGGCAMCTGCCACC | | GGCXAACTTTTGTATTTTTAGTAGAGA | AGCCTGGCCAAGATGGTGAAACCCCGTCTCTACTAAAAATACAAAAGTTAG |
| 301 | 587 | AGATGGTGAAACCCCRTCTCT | P | GATTCTCCTGCCTCAGCTTCC | | TCCTRAGTAGCTGGGATTACAGGCA | AAAAGTTAGCCGGGGGTGGTGGCAGGTGCCTGTAATCCCAGCTACTYAGGA |
| 302 | 589 | TCACATCGGAGACAGACCTATAATC | P | CAATGTAATTCACTGAAAGYATTCCTAG | | CAGAGCTTGGACTAAXGACTTGCCCTA | CAGGCTCCCATATGTGAATACCTAACTAGGGCAAGTCCTTAGTCCAAGCTC |
| 303 | 590 | TGCTGTCGTGGTCTTCCTC | | CATTTCTTACCAATTTCCCCAAT | P | ATAGGATTACTCACTCATTCACGCA | ATAGGATTACTCACTCATTCACGCACTCATTCATTGGCCAGATCTGTAGTT |
| 304 | 591 | CAACACCTTTATCCTTTTCTTCGAT | P | TCAATTCATGCCAAAAATATCATG | | TCATGTAAGATGAAAGTGAGGTATA | AAGGTCCTGGGGATACCTTAACCTCGTATACCTCACTTTCATCTTACATGA |
| 305 | 592 | TCACTGCAACCTCTGCCTC | | CAAAAACTAGCCASGTGTGGTG | P | CAATTCTCTTGCCTCAGTCTCCCAA | CAATTCTCTTGCCTCAGTCTCCCAAGTAGCTGGGATCACAGGCACCCGTCA |
| 306 | 593 | GGGTTCAAGCAATTCTCTTGC | | CATGGCAAAACCCCGTCT | P | GGATCACAGGCACCCGTCACCACAC | GGATCACAGGCACCCGTCACCACACGTGGCTAGTTTTTGGATTTTTAGTAG |
| 307 | 594 | CGATCCTTTACCACATCCTTCTT | P | TGTGAGATGATGGCTATGTTCATT | | TTGTTCCACTGTAGXAATCATTTTACC | AACATGATGTTTTAAGACACATATACGGTAAAATGATTACTACAGTGGAAC |
| 308 | 595 | CTTGGAAAGCAGGTATATGGAAGG | P | TCTGTGTGTGTGTGCCTGTGT | | TCATTTCACTAATGTTGGCTCCTCT | GTTATCTCAACTTCACATTAAACATAAGAGGAGCCAACATTAGTGAAATGA |
| 309 | 596 | TAGATACTAATAACTTCTATTCTCTGATGCATTG | | GATTGAGGCTACAGTGAGCTGTG | P | TAGTAGGGCAGACATXAAGCATTTCAT | GTAGGGCAGACATTAAGCATTTCATGTGCATTTTTTTTTTCTTTTTGAGAC |
| 310 | 598 | TTCCCAAACTACTTACCGGAGC | P | CTTGGCCTCCCAAAGTGTT | | GATTTTTTAATGTCTTAGATGGAGC | ACAATAGGAAGAACCAGGGATTGCACGCTCCATCTAAGACATTAAAAAATC |
| 311 | 599 | GCCCCTGTAGTCCCAGCTA | | TTATTTTTTTATTGAGACAGAGTCGCT | P | TTGGGAGGCTGAGGCAGGAGAATGG | TTGGGAGGCTGAGGCAGGAGAATGGGGTGAACCCCGGAGGCGGAGCTTGCA |
| 312 | 600 | CATGCATAACTCTGACAGGAAGA | P | GGGACACCCAAAAGCTGAA | | AAGCACAGAGGGGTTGGCGAGGAGT | GCCCCTGGGGAGGGAGAGGTCCAGGAACTCCTCGCCAACCCCTCTGTGCTT |
| 313 | 601 | GTGTTTAATACCGTTTCTTCATCTATAACATAA | | TGCCACAGAGAGACTTCTTTTTTT | P | TAATGATATAGGAAGCCACTCAAAT | TAATGATATAGGAAGCCACTCAAATGAGGCAGACATGTTGCGTTGCGCTTA |
| 314 | 602 | TAATGGGTGTCTCCTTATGATATCCA | P | CTTTTTATACTCCACTCTGCAAGCG | | TATGCAGAGTTCTGGAAGAATTCCC | TTTGATGGCCTTGCTAGCTCAGTGAGGGGAATTCTTCCAGAACTCTGCATA |
| 315 | 603 | TCGGCCTTCCAGAGTGCT | P | GAAATTTTATCATGAGCCAGATGC | | TCATCATTGAAATTAGAXCTTCTGGCT | GATTACAGGCGTGAGCCACCGCGCCAAGCCAGAAGCTCTAATTTCAATGAT |
| 316 | 604 | CTTGCAGTTTCTTCCTTTGTTCTACT | | GAACACAATGATGCCAAAAACC | P | GTTGTCAAGTTTAATCCTTCCTCCT | GTTGTCAAGTTTAATCCTTCCTCCTGCAAACTCCCTGAGGCAGACTCTTTT |
| 317 | 605 | ATTACAGGCGTGAGCCACC | P | GTGTTTCTCCAGGACCGAATC | | CATGAGCCAGATGCTGAGGAAGAGA | AATTTCAATGATGATTGTGCTTTTTATCTCTTCCTCAGCATCTGGCTCATG |
| 318 | 606 | TAGTGTGGATTCTCAAGTTTTCTCCT | | CTTGTTAGCTGCCTTCCTTTACC | P | ACTTCCATCATACAGTCTTCAGCAA | ACTTCCATCATACAGTCTTCAGCAACCTTGAAAGATTGGACAAGCTTCAGC |
| 319 | 607 | AAGTAATCCTCCTGCCTGAGACTC | P | ATTTCTTGAGCCCAGGAGATTAAG | | ACGAGACCCCATCTCTACAAAAAAA | CTACCACACCCAGCTATTTAAAAAAATTTTTTTGTAGAGATGGGGTCTCGT |
| 320 | 608 | GCAGCATTTTTCATAAGAGCTAAACA | P | TAGCATAATGTTTTAGCACACATTGG | | CACATTGGTAGTTTATTTCTTCTTA | ACATGGAATAGAATATCACTTAACTGTAAGAAGAAATAAACTACCAATGTG |
| 321 | 609 | CGTGTACCGAGAGCTGTTTT | P | CAGTCCTCTTGGTCTGGAGAGG | | GAGAGGATGGGXCTGGXCTGGTGCCAC | TCCTAGATCCCTCAGCACCTCTGTGGGTGGCACCAGCCCAGCCCCATCCTC |
| 322 | 610 | CAGGAAGGTGGGGAAAAGTG | | CAGACAGGAAGCAGGGGC | P | CGACTGGGCATTGGCAAGTGAAGGG | CGACTGGGCATTGGCAAGTGAAGGGCCCTGGAGGCGGGGAGGGGGCATCTC |
| 323 | 611 | TTTTTTTATATTTGGAGTACTGCTCAACA | P | ACATGGCTCAAGATTCTATCATACAAC | | TATCATACAACATCTXCTCGCATTCAA | ACTGACCTTGGCGTGACTTTGGCCAGTTGAATGCGAGCAGATGTTGTATGA |
| 324 | 614 | AAATGTGTATCAAACCACAATCCTCT | P | GTTTCTGGCAGAATGTTCCAAA | | ATAGGAACTAGCAGCCAAAGGACAA | CACTCCTGACTCGGTCATTTCTGACGTTGTCCTTTGGCTGCTAGTTCCTAT |
| 325 | 615 | TAGGGAACCACTTACTACTCATAGAATCAT | P | GTTTCTATCTTCATTTGTTTCTATACCCTTT | | CAATATGTAAGATGGAXAAGATTCTAT | AAGAATTTGCCTGGAAGCAATCTCAGATAGAATCTTCTCCATCTTACATAT |
| 326 | 616 | TTTTTTTTTTGTTTGGAGATGGAGT | P | GGAGAACTGCTTGAACCCAGA | | CCAGAAGXCAGAGGTTXCAGTGAGCCA | CAGGCTGGAGTGCAGTAGTGCAATCCTGGCTCACTGCAACCTCTGCCTTCT |
| 327 | 617 | TTGCACATTTTTCCCAATGAA | P | ACTTGAGAGCAGCGTGATTCC | | TGAAGAAGGCATCTCTGGATAATGA | TCATCAGGACGCTATTTCTTATGCTATCATTATCCAGAGATGCCTTCTTCA |
| 328 | 618 | GAAGTCAGGGTGAGGGGACA | | CGCCATTGCACTCCACCC | P | CATTTTTTTTTTTTTTTTTTTTTTT | CATTTTTTTTTTTTTTTTTTTTTTTGTGAGATGGAGTTTCACTTTTGTTGC |
| 329 | 619 | TTGCTTTATCATCCCTCATCA | P | GTTTTAGAACAGGGCTAAAATGGTC | | GAGAGAXGGTGACAXGGAGCCCAGGGA | ACCCTTTGTCATAGCTGCCCCCTTCGTCCCTGGGCTCCCTGTCACCCTCTC |
| 330 | 620 | ACTAAAAATACAAACTTGAAAACATCATGG | P | CAAAGTCCTGGGATTACAGGC | | GGCTGGCTCAATTCTTTTGGCACAA | GAAGAAGCCTCTGGGATCAAAAATAGTTGTGCCAAAAGAATTGAGCCAGCC |
| 331 | 621 | TATAATGGAGCAAGTCTTACTTTGTGAG | | GAAACACTGGTCCCATTGGAT | P | TATTCAAAAGCTAAATGTGGGTCCT | TATTCAAAAGCTAAATGTGGGTCCTGTGAAATGCTTTCCCATTCAAAAGCT |
| 332 | 622 | CTGTTAGGAAAAAGTTCACTCCTCTCT | P | ACCTTAATTCTCTCCTTAAAGGCCC | | GGCCCTATCTCCAAATGTAGTCACA | TTATATGTTGAAAGTCTAGCTTCCAGTGTGACTACATTTGGAGATAGGGCC |
| 333 | 623 | TTTCCTTTCATTTCTTTTCTTTGAGAT | P | GAACTTGTAAGGTGCAGGTTGC | | TTGCXGTCAGCTGAGAATGAGCCACTG | CGTCTCAGTCTTCCTAAGCTGGAGCGCAGTGGCTCATTCTCAGCTGACTGC |
| 334 | 624 | TGCAGAGCCCATCTCCCC | | GGCCTCCCAGAGCCTCAC | P | CTTXCCTGCAGCAGXCTGGTAGGGCAC | TCCCTGCAGCAGCCTGGTAGGGCACAGGCATTGCCACTCTCTAAGAGGACA |
| 335 | 625 | TAAAAAAGATGCTTCACATACACCCT | | GATTTTCTCCCCTACAGGACACC | P | CAAGTGCAGGCAXACAGTGTGACAACC | AGTGCAGGCACACAGTGTGACAACCGAAAATGTCTCTGACATTGTTAGGTG |
| 336 | 626 | ACATAGTAAATGCTCAGTAAATGTAGGCA | P | CTCTTAATAGCAAAAATAAAATATGAGCTATAGG | | GACCAATAAGGCAAGAGXCCAGACATA | TTAAGAGGCAGACGGAGGGCCTGCAGTATGTCTGGCCTCTTGCCTTATTGG |
| 337 | 627 | AGATCTCAGGAGGAGGGCTG | P | GTACCTTTCAAATGCTGGCC | | GGXCCAGAAAGGTGAGGCAAGGAGGGG | GGGATTCACAGAGATGGAGGCCAGGGCCCCTCCTTGCCTCACCTTTCTGGG |
| 338 | 628 | AAGAGAAATAACTAGTCTTCCTGTCTCAGG | | GAACGAGAGATAGAAAAACTGAATAGTAGTTG | P | TGGGAAAAATATCACATATAAGTGG | TGGGAAAAATATCACATATAAGTGGATACATGCAGCTCAATCCCACGTTGT |
| 339 | 629 | ACCAACTAGTGCCAAGCGC | | GAATTCTGGAGACACGCTGC | P | ACAGCTATGACXCTGCCTTCTGAGAGG | AGCTATGACTCTGCCTTCTGAGAGGCTTTCTGGAAAGAATGAGTTCTCTGG |
| 340 | 630 | TTGGGTATTTGTTTATAGCAACACAA | P | GAGGTTCCCCAGCCTTGT | | TCCTCCACTCCTCCTTCTTTCCCCC | ACTAACATGGGGGTGAGGTTGGAGCGGGGGGAAAGAAGGAGGAGTGGAGGA |
| 341 | 631 | CAAGCACCTGTCCACGGT | | CTTATACTTTCCTTTCTACTGCGGG | P | CTGXCCAGAGCACAXAACGGGGTTCCA | GCCCAGAGCACAGAACGGGGTTCCAGAGTGCACTCACCTCCCCTCTGAACT |
| 342 | 632 | TCTAGCCTTAGGGTACCTTCCAAG | | GATATCAAACACAGGACTTAACCCA | P | TGTGACCXAGATATATTTGTGGCTTCT | TGACCCAGATATATTTGTGGCTTCTCGTCATATTTGCCTTTCCAAATTCAG |
| 343 | 633 | TTTTCTGGACTAAACTGCTGCG | P | CAGACTCAGAGAGATTAAGTGACTGGA | | GTAAACAGTAGAGCCAGAGCCATAA | ACATGTAACAGAAAGAACAGTTATAATTATGGCTCTGGCTCTACTGTTTAC |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 344 | 634 | AGGACTAACCCCACATTGGG | | CTTGACTAGTTCCCAGTCGAAATTT | P | CCCCAGTCATGGGGTGATTGTCCTT | CCCCAGTCATGGGGTGATTGTCCTTGTTGAGCCCAAGGAATGATGGTGTTT |
| 345 | 635 | AACAGACAGACCCCCACCC | P | CAACCCCTTTCTGATTTCCC | | CACAGCCACTCGGCTTCCTTCACTC | GCAGCCTGCTCAGGGAGCCAGGGCAGGAGTGAAGGAAGCCGAGTGGCTGTG |
| 346 | 636 | TGCAGACTCCCGCCCAGG | P | GCCAGTTGTTGAACGTGGG | | GGGGTTGTGTGACTCAGAXCCTGGGCT | CCACACTGCCAGCTGGGATTGGACAGAGCCCAGGCTCTGAGTCACACAACC |
| 347 | 637 | CAACAGACATTGCATTGGCA | P | TGGCTTAGAACTCAGAAACCAGG | | TGACTGTAGTTAAATAATCTCCTAT | TTGCTTTTGGTTTTCAGCTGTAATAGATAGGAGATTATTTAACTACAGTCA |
| 348 | 638 | TGACCCCTACAGACACTTAGTTGTG | P | GTGATGGTGCTGACGTAGGATT | | ATTTXGGACTATCAATCCCTATGTC | AGAAGGCAGTTCTCTAGAGTGGAAAGGACATAGGGATTGATAGTCCTAAAT |
| 349 | 639 | GCCTCCACTTTTGGACTGACT | | AGAGCTTGCTTTAAAAATGCCAC | P | ATGTGAGAAGAXTTCCTAAXTTACCAC | GTGAGAAGAATTCCTAAATTACCACGTATGAAATTAACGTCCATCTTTCTG |
| 350 | 641 | TTTAAAGTGGCCCTGCTGTTAC | | GATTACAGGCATGAGCCACC | P | CCAGCGGXTTTAGTCTCAGGTAAACCA | AGCGGTTTTAGTCTCAGGTAAACCAGTCTTGGTCATGATTCTCTGTCTTCA |
| 351 | 643 | TTAGGTGTTACAAGTGATCTGGAGATG | | TCTATGGATGCTCAAGTCTCTGATATG | P | TTAAAGTATGTGGGAGAATGCGGGT | TTAAAGTATGTGGGAGAATGCGGGTGGTTTATATGCAAATACTGTGAAGGC |
| 352 | 644 | TTTTTTTTTTTTTGAGACAGAGCAGT | P | GCAGGAGAATCACTTGAACCC | | AXCCCGGAGGCAGAGGTTXCAGTGAGC | CTCTGTCACCCAGGCTGGTGATCTCGGCTCACTGCAACCTCTGCCTCCGGG |
| 353 | 645 | ATCCCCCTCTCTGTCACCC | P | GGTACCAGGGAAGATGAGGG | | GCCCAGGAGGTGGAGGTTGTAGTGA | CTGGAGTGCAGTGGCATGATCACGGGTCACTACAACCTCCACCTCCTGGGC |
| 354 | 646 | TTGGGGGGAGGCAGCCAT | P | CTCAATGGAAAGTCCCGTAATG | | AGGATTAAGTGAGATGGTGCCTGGT | GAGCACCTGCTCCTCACCAGGCATTGACCAGGCACCATCTCACTTAATCCT |
| 355 | 647 | GAACCCTGCGAATACACCCT | P | CTCATCCTCCCACCTTGGC | | TTAAAATGCTACCGTATAATGTATG | GAGTCTGAAATTTATTCACACATATACATACATTATACGGTAGCATTTTAA |
| 356 | 648 | CCCACTGGAAGGTGAGCC | | CAATTAACCTGGACACCGCC | P | CAAGAGACTGGGCCAACACCGAGCA | CAAGAGACTGGGCCAACACCGAGCACGGAGGGGATCAGAGCGTGTGTGTGT |
| 357 | 650 | AGTCTCTCCGCTTGGGTCTT | | GGGTTCTGAGCCCATGATATC | P | CACTGAGCACGTGATTCCCCACACC | CACTGAGCACGTGATTCCCCACACCGAGCGAACTTCAAAGCTCCCAGTGTA |
| 358 | 651 | TTGTGTGTGGAGACACTGAGC | P | GCTGAAAGGGAGGTGTGATTT | | ACACAGCCACGATACAATGTCAGCC | CCCACAACTGTCTCCTGCAGCATGAGGGCTGACATTGTATCGTGGCTGTGT |
| 359 | 652 | TGCTCCAGAATCCAAAACATTT | P | TGAGCATCCCCAATCCAA | | TCTGAAATTTAGACTGCTCCAATGA | ACCAAAATGATGTTCAAAGGAAGTGCTCATTGGAGCAGTCTAAATTTCAGA |
| 360 | 653 | GTCCAAAATTAATCTAACTGATCCAACTT | P | AGGACCTAACTACGTGTTGTCTACAAG | | ACAAGCAATGCACTTTGAATATAAT | CCCTCTACTTTTCATCAAGCTGACTCATTATATTCAAAGTGCATTGCTTGT |
| 361 | 936 | CTCATGAACCAACAGTATAGAAGAAATAATT | | TCACTGTCAGTGGCTCTAATTAAGAAT | P | TGGTGCGATXTGGGCAAACXAGAAAAA | GTGCGATTTGGGCAAACTAGAAAAAGMCAAGAAAAATGAAAAGATCTTTTT |
| 362 | 937 | TGATTTTCCATACAAGCTCACATATAC | P | AAATATAACTGAGATTGGCTAACAGCTT | | TTAAGACCGAATTCTCTCXAGGCAAAC | CCATGAATCCGAGACTCGAACAGATCGTTTGCCTAGAGAGAATTCGGTCTT |
| 363 | 938 | TCTAGTGCTGAAATTTTGGTGTGA | | CAATAGCATCCTATGATCCAGCC | P | GAATTCCCTAGGCAGAAAAAAAGGA | GAATTCCCTAGGCAGAAAAAAAGGAGAGGTAGAAGGAACAGCATATTCTAA |
| 364 | 939 | TCTGAAATTTTGGAACAYACTGG | | GTATGTGCTTAATTCCTCCAGCA | P | GTCTCTAATGAGTTTTTTCTGGTAG | GTCTCTAATGAGTTTTTTCTGGTAGGCAATGTTTTACATGTGTTGTCATAG |
| 365 | 940 | GCAAACAAGCCTGTGGTATAAATT | P | TCCCAATCCAGTAGACGCAG | | AACTGTGCATATAAGAXTTXAATGAAG | TTTATCCACAGAAAGCAGACTGCCACCTTCATTAAATTCTTATATGCACAG |
| 366 | 941 | TGAAAACCAAAGCATTGATAGGG | | GCCAAAAAGGCAACAGGG | P | TGCATTGAGTTGTTGGCAGAATTTC | TGCATTGAGTTGTTGGCAGAATTTCGTTCCATGGTGCTGTAGGATTGAGGT |
| 367 | 942 | TAGCTGGGATTACAGGCGC | | GATCACTTGAGGCCAGGAATT | P | AATTTTTGTATTTTTAGTAGAGACG | AATTTTTGTATTTTTAGTAGAGACGGGGTTGTGCCATGTTGGCCAGACTGG |
| 368 | 943 | ATTACAGGAGTGATTCCAGGTGC | | GTCACACAGTCATGGAGACATAATACC | P | TCTGTGGGAACAGAGAGAGCATCAC | TCTGTGGGAACAGAGAGAGCATCACCGTAGTTCAAGCCAGGCTCCTTTAGG |
| 369 | 944 | TGCTGGGATTACAGGCATG | P | AACCTTTGGCTAAAAGGGTCTG | | CTGATTACCCAAAGAGATTAGAAAC | GCCACCATGCCCAGCCGCCAAGAGGAGTTTCTAATCTCTTTGGGTAATCAG |
| 370 | 945 | CTCCACATTACCAAGAGGATAGGTC | | GTAAAATGCTCAGCTCAGATGGA | P | AAAGCACCAATAACAACAGTAGCAG | AAAGCACCAATAACAACAGTAGCAGCTCATATTCACTAACTGCTCAACATG |
| 371 | 946 | ATCAGGAGCACTTGAGCCC | | GACAAGGCGAGACTCTTGTCTC | P | ACCACATCCTAACATCGTAACAAAA | ACCACATCCTAACATCGTAACAAAAGGAGACCCCCATCTCTACAAAACAAA |
| 372 | 947 | CTGCAATTCCTGCCAAAAGT | | TGGCTACTGTTGCTTTACACTGAA | P | AAAGATTATTGGAAAAXTTGACAAG | AAAGATTATTGGAAAAATTGACAAGATGATTTAAAATTATATAGAAATACA |
| 373 | 948 | ATATGACAGCTTGACATGATTACGAA | P | CTTTAGGATAGTAGGGCCTGCTC | | GTGAGXGCTGGTGCAGACAGGACCC | GCTTATTCCAGATAGAAGCCGCCAGCGGGTCCTGTCTGCACCAGCCCTCAC |
| 374 | 949 | TCCATGTTGACCAGGCTAGT | | AGTAAAGAGAGAGAACACAAAAGAAATTTTT | P | TCTTGAACTTGTGAXCTCAGGTGATCT | TTGAACTTGTGACCTCAGGTGATCTGCCCGCCTCGGCCTCCCAAACTGCTG |
| 375 | 950 | AGGAGCTGAGGGATCTGGG | P | TAGAGAAGATGCAGAGAAGAGGAGAC | | AAGAGGAGACCCXTGCAAAGTCATGCT | GTGTCCCATCTTGGCCACTATTCACAAGCATGACTTTGCATGGGTCTCCTC |
| 376 | 951 | AAAAGGAGATCGCAGTTCGA | P | GCGTGGAATCTTGATTCGTG | | TGAGAAGGAGGGAAGAGGTTGTTTC | CCGATTCCCTCTCCCCGCCGACTCTGGAAACAACCTCTTCCCTCCTTCTCA |
| 377 | 952 | ATGCACACACCTTGCATGG | | AATAGTCAATCTGCATCCATGTCC | P | TCACAAGGGGGCTCCACCAGACTCA | TCACAAGGGGGCTCCACCAGACTCACCACCGAAGAAATGCCAGCCAACAGC |
| 378 | 953 | CAGGTGATCAGGAAGGACACTAG | | GTGTTTTAGGTCATATTTCTTGGGG | P | GTGGATTTATATGAAAAAGGAAAAC | GTGGATTTATATGAAAAAGGAAAACGACATGCAGGCTGTCTGTACTAAGCC |
| 379 | 954 | GCCTTTCTGCACCTAATTCATG | | TGTTCAAAATATATACTGAGGTCACTACTGA | P | CCCAAGATTTCCTCACTCCATAGTA | CCCAAGATTTCCTCACTCCATAGTAGAGTAGTTTTAAATTTTCAGTAGTGA |
| 380 | 955 | GTTCTATATAGGCAAACTCATTTGGACA | P | ACGGTTACCATCCCAAAGTCTAA | | TACCATCCCAAAGTCTAAGAAAAAT | CAATTTTATCTTTGAATGTTCCTTTCATTTTTCTTAGACTTTGGGATGGTA |
| 381 | 956 | TGTGGGTTTTTTTTTAACTTGCC | P | GCCAATGGTTGCCAGGTT | | ACGGAGXCTGCTGGCTTTCAAGTCTAC | TTTCATTGTCCCTCCACTGATCCACGGTAGACTTGAAAGCCAGCAGTCTCC |
| 382 | 957 | CTTAGTAAGCAACACAAAAACATTGGT | | GCGCCACTGCACTCCAGC | P | AAGTAXACXAAATAGTATGAAATAAAA | GTATACTAAATAGTATGAAATAAAAGTCTGTTTAAATTTTTTTCTTTTTTT |
| 383 | 958 | ACGGTCACTTGAACCCTGGA | | GATCCATTTTTAATTGAGAGATTTCTG | P | CTGTTCTCTAGCCTGGGTGACAAGA | CTGTTCTCTAGCCTGGGTGACAAGAGCGAAACTCCATCTGAAAAAAACAAA |
| 384 | 959 | ATAATAGAACATCTAAAGTCCAAGAAGAGT | P | TCTTCCTCCAATTCCCTCTGTAT | | TCTGTATGCTXAACTGTTTTTGAATGC | TGGGCGAGGTTCATTGGGAAATTAAGGCATTCAAAAACAGTTGAGCATACA |
| 385 | 960 | GTACCCATGAGATCTTTCACCTACAC | P | TGTCTTAAATCCTTTCACTATAAGGACC | | ACCCTTXAAAGTTGCCTAAGTTGAAAT | ATCTAATAACTGAATAATGGCAATTCATTTCAACTTAGGCAACTTTGAAGG |
| 386 | 961 | GAAAAACATTTCCACTGAAAACCA | P | ACCGGGGATCTCTGGGAT | | ACCGGGGXTCTCTGGGXTCAGGTGAGT | TGGGAGAACTTCAGCTTTTTTTCCTCACTCACCTGATCCCAGAGATCCCCG |
| 387 | 963 | GCCTTTCCTTAACTAGCCTGTAATCT | | ACGATTAGCCAGACTGAATGCA | P | GTAAGTACATCTTACATTTTTATTA | GTAAGTACATCTTACATTTTTATTACCTTTAGCATCTATTAGCACAATGCA |
| 388 | 964 | ATCTAAGGCTCCAGGGTCTCC | | CTTGTGAACCCCCTCACCA | P | CAGCTCTGTGTXAGACTGAAGACCCAA | GCTCTGTGTCAGACTGAAGACCCAAGGCCCTGGTGAGGGGGTTCACAAG |
| 389 | 965 | CTGCTTTAAACAGTGGCTGAACTAA | P | TGGGAGGCTGTGGAGAAA | | GGCTGTGGAGAAAAGGGAACATTTA | GCACCAATTATGTTTAAATGTTCCCGTAAATGTTCCCTTTTCTCCACAGCC |
| 390 | 966 | GTACTCAGGTTAGGTGTGGTTCAC | P | ACTTACCCAAGTCCATATCTTAGGTTATCT | | TTAGXTTXTCTTTATAACCCTACACAC | TCACTTTTGCTTTAAGGGAATTCCTCGTGTGTAGGGTTATAAAGATAACCT |
| 391 | 967 | GAGCTTTAGAGGAACTAGACTTTCTATCCT | | AGGCCATCACCATCTAAACCTT | P | GTGTTGATTCTTCTTTTTATCCCAA | GTGTTGATTCTTCTTTTTATCCCAACACTTAACGTGTGAATACATCCTGAC |
| 392 | 968 | ATTAAAGCAGTTTCCTAGCGTGTG | P | CAGCCAAACCTGCCTTCC | | TCTGCCAGCCAAACCTGCCTTCCTC | AATGCTTTCACATGAAGGGATATTTCGAGGAAGGCAGGTTTGGCTG |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| | | | - | | - | | |
| 393 | 970 | CATCCCCCATAGTCCTGCTC | | GAAAATGTGTTGGGAAAGGCA | P | GCTTCTTAGGCAAACATTTCTTTTT | GCTTCTTAGGCAAACATTTCTTTTTGGTTTGAGGCTTTTATAGCTGCAGGG |
| 394 | 971 | TGGAAAATATGGGAAAATGGTAATG | | GGATCTTTCTGGYGCCCA | P | AACAAGTGGTTGAGCAGGGGAGGGG | AACAAGTGGTTGAGCAGGGGAGGGGGGTCATATCTGGGCRCCAGAAAGATC |
| 395 | 973 | TGCCTTGAAGTGTTTTTGCTG | | CTCAAATAAGAGCTGTGTGGCC | P | CAGAGAGGTCCAGCCACTTGCCCAA | CAGAGAGGTCCAGCCACTTGCCCAAGGCCACACAGCTCTTATTTGAG |
| 396 | 975 | GGCCTAAGCCACTTGTCCTG | | ATAGCTGCCTCTTCCCTTTTATAAG | P | CTGCATACTACATAGGTAAAAGATG | CTGCATACTACATAGGTAAAAGATGGGGACAAATACTTTCTATTTGCTTAT |
| 397 | 977 | GTGAGTAAATACAGAAACAGATGGATATTTT | P | ATGTCCATTACAGATTAGCCCACA | | AGCCCXCACTTAAGTTATTGCTGTGAC | ACGGACAACAACAGTGAAAAGGATCGGTCACAGCAATAACTTAAGTGTGGG |
| 398 | 978 | ATTTCCTTCCTAGAAGGTCCCAG | P | GATATTTAAGCAAATACTGTAGGATAACAGCT | | ATAACXGCTGAAGAGGCTGGAGAGAGG | CTGTGATTCTCTTTCCTATCATGTCGCCTCTCTCCAGCCTCTTCAGCTGTT |
| 399 | 979 | CAAAGGAATGTATCCCTCACTCC | | TGCTTAGTTACTGGTTGTCCTGAAA | P | AATTGCACCCCTAGAAAACCTATTT | AATTGCACCCCTAGAAAACCTATTTCATGGCATAATTTTTGTTCTATTACT |
| 400 | 980 | GTGTGGCTAGGAGAGAGATGCA | | TGTCCAGGGGAAAATATGTTCTG | P | AAGAATATTAGGAAAGCAAGTTGAA | AAGAATATTAGGAAAGCAAGTTGAAAACTTCAGGAAGAAGAATGAAAATCA |
| 401 | 981 | ACTCGTAGCACCTTCAATGGTATAAT | | CAGGAGGAATGAGGACCTTTAAG | P | AGACTTTCACACTGTTCTCTATTGA | AGACTTTCACACTGTTCTCTATTGACGTTCTCTTCTATAGTGTTGATAATA |
| 402 | 982 | ACCAGTAGCCAGCAATTCTGC | P | CAATAACAAACAGTGAGAGTCATCCT | | TGCCAGXGCTGTTCGCCTATTCAACCC | CTGCCTCTAGAATAAATGGTTACCACGGGTTGAATAGGCGAACAGCCCTGG |
| 403 | 983 | GCAGAATTCACAAATATATAACCTCATAATT | P | TCATGCTTAAACATCAACCTTGTG | | TGTGAATARAGTAGTAXGAAATCTTGA | ATATATAACCTCATAATTCATCGACGTCAAGATTTCTTACTACTYTATTCA |
| 404 | 984 | CAGAATTAGAACTGGTATATGAAGAGAGTAGC | P | GGATCAAGGACAACTCCAGGA | | AATAXTAXTATXAAATTATTGAATGAT | GTATATGAAGAGAGTAGCCCATGGAAATCATTCAATAATTTGATATTATTA |
| 405 | 985 | TATATAAGCATACGTTGGCCCAAT | | CATTTGAATATGTCAGCCTGAGG | P | GATATATAAGCATACGTTGGCCCAATG | TATATAAGCATACGTTGGCCCAATGGTATTAATTTGCTTATCCATACTAAT |
| 406 | 986 | AAGGTTTATTTCAGGCCCATTATAG | | GTGTGGTGCTGCAACAGC | P | TTATTTCAGGCCCATTATAXCTTTCCA | ATTTCAGGCCCATTATAGCTTTCCAACTGATCTCCTGCATTCCTTTTGGTT |
| 407 | 987 | TGCAGTGTCATTTGGTTCACTT | | GATACTATTACAAGTTGTTAGGAAACAGTAAATTA | P | GGATCTGCAXTGTCATTTGGTTCACTT | GTACCCGGGGATCTGCAGTGTCATTTGGTTCACTTCGCTACTACTGAA |
| 408 | 988 | CCTGACCGAATCCCTATCTTCT | | AGGAGAAAACGTATGTAAAGGATTTAGTAGA | P | TCTTAGAXTTGAGAAATAATAATTG | TCTTAGAATTGAGAAATAATAATTGCTTAATTTTAATAAGTTTCTACTAAA |
| 409 | 989 | CTGGACTGGATGGCCTCTG | | CACACCTATTTCCTGTAGGTTTTAATTATTT | P | TTTGGGGCAAAGCTGGAAAATGAAA | TTTGGGGCAAAGCTGGAAAATGAAAGGATTTCATTTGGCAAATAATTAAAA |
| 410 | 990 | ATTCCACCTGAATGCACACTG | | GATCTCCTGGAACAGAATGCTATG | P | CAAGACCTCAGTATCTGCTTCAGTG | CAAGACCTCAGTATCTGCTTCAGTGGTGTAACTGTGCACCTGCAGCCATAG |
| 411 | 991 | AGCGGCAACCTGGTCCCA | | CTTTCAGAGGCAGATCTCGG | P | GCGGTGAGGCAGGAAATGGGTTGTT | GCGGTGAGGCAGGAAATGGGTTGTTGAACAGGGAGAAGGTCAGGAGCCGTG |
| 412 | 992 | AACAGAGTGAGACTCCGTGTCAG | | CACACTCAGGGGGCTTCA | P | AAAGACAAAACTAAGCCTGAAATAG | AAAGACAAAACTAAGCCTGAAATAGCTCTTTCTGGGCCTCCCCTTTGCTGT |
| 413 | 994 | ATCCCCCTCTCTGTCACCC | P | GGTACCAGGGAAGATGAGGG | | GCCCAGGAGGTGGAGGTTGTAGTGA | CTGGAGTGCAGTGGCATGATCACGGGTCACTACAACCTCCACCTCCTGGGC |
| 414 | 995 | TTGGGGGGAGGCAGCCAT | P | CTCAATGGAAAGTCCCGTAATG | | AGGATTAAGTGAGATGGTGCCTGGT | GAGCACCTGCTCCTCACCAGGCATTGACCAGGCACCATCTCACTTAATCCT |
| 415 | 996 | CCCACTGGAAGGTGAGCC | | CAATTAACCTGGACACCGCC | P | CAAGAGACTGGGCCAACACCGAGCA | CAAGAGACTGGGCCAACACCGAGCACGGAGGGGATCAGAGCGTGTGTGTGT |
| 416 | 997 | GCAGGAGACTCGCTTGAAC | | GTTTCACGCTTGTTGCCC | P | CCTGCGAGXCGGAGGTTACAGTGAGCC | TGCGAGGCGGAGGTTACAGTGAGCCGAGATCGTGCCATTGCACTCTAGTCT |
| 417 | 998 | CTGGTGAAAATTAAGTTAGCAAATGAA | | CCTTTATTAGAAAGGAGAGTTAAATGTTGTATAC | P | CACTTCCATATGGTTTCTTTTCTCC | CACTTCCATATGGTTTCTTTTCTCCGACATGGGACTATTCAGTTGACCTTT |
| 418 | 1000 | CGTCCTTAATTTGTTCTTTGTAGCA | P | ACTGAAGCCTGCCAATGAAC | | CATGCAATACAXATCATTTACTAATAT | TGGTGCAGTAGAATAGACCAACCTCAATATTAGTAAATGATTTGTATTGCA |
| 419 | 1001 | TCCCCAGACATGTGGAATTG | P | CATTTTTAGATGTCTTTACAGCAATGC | | GCTGATAAAGACATAACCXAGACTTGG | ACTAAACCTCTTCCCTTTATAAATTACCAAGTCTTGGTTATGTCTTTATCA |
| 420 | 1002 | AAAAATGCTGGGTGAAAGAAGC | P | CAATCGGGACTCCTACCAAATT | | ATTCCCATCCAGXTTTACCAACAGGCA | GAAGTAGAAGATGGATCATTGGAATGTGCCTGTTGGTAAACCTGGATGGGA |
| 421 | 1003 | CCAGGAGTAGGGCATTGCTAT | P | CCTCATCTTTCTGTCTTTTTCTAAGC | | AAACTGTTCAAATCTCTGCCCATTA | AAGATACCTGACACTTTAAAACTGGGTAATGGGCAGAGATTTGAACAGTTT |
| 422 | 1004 | GAATCACCTGTCTGGGTCTCAA | P | GATAATTCAGAGAAGGATTGTCCACA | | ATTGTCCACXTTAAAATGXTCCCTTAC | AATGGAAGTGCTTTAGCTTCACTCAGGTAAGGGATCATTTTAATGTGGACA |
| 423 | 1005 | GCATTTCTGAGTCCTCCTCAAG | P | AATTTTCAATGAGATACTGGCTTCTATTT | | GGCTTCTATTTTGCTTATTGGTTTG | AGAGTCAGGCAATCCTCAGTCATGTACAAACCAATAAGCAAAATAGAAGCC |
| 424 | 1006 | TTAAAATAACTACAGTCATTCCAGTGGAC | | TTTAGATAAAATCCAAAACTCTTCCTCTC | P | CAGATGCAAGTYGGAGAACCXTCAGGC | GATGCAAGTYGGAGAACCCTCAGGCGGAAGCTGAGCATAGTAAGAAATTGG |
| 425 | 1008 | AATTGGCTGATGCAAAGAAGAA | | GACAAATGACTTACAGATCCCCC | P | AAAAAGGTACATCAGAAACAGAAAC | AAAAAGGTACATCAGAAACAGAAACGTGCTACTATCAGGGCAACTGAGCTT |
| 426 | 1009 | AGGTGTGAGCAGGGAGTGG | P | GGAAATAGATATGGAATATTTCAAGAATCA | | TGTGCAGAGCTCTGAYGGCTGGTGA | TGGCTGAGGCTGGGCAGAGCACAGGGTCACCAGCCRTCAGAGCTCTGCACA |
| 427 | 1010 | TTCCAGCTCTGGGACCAAG | | GTGCAGCCTCCTGGAGAAC | P | GCCAGGCGTCCATCACTCCCTCTTC | GCCAGGCGTCCATCACTCCCTCTTCCGGAGCTTCCATGGAATGACGGCCTG |
| 428 | 1011 | TTAGCAGTGGCAGGTTTAACATTC | P | GCTAAGAGTTTTTTCTAGTGTACCAGCC | | AGTGTACCAGCCTCACAGCXTGATTCA | CATTTATAATTGCTGAGTCATGAATGTGAATCATGCTGTGAGGCTGGTACA |
| 429 | 1012 | TGGAGTGCAATGGCGTGA | P | CCTAGCTGCTTGGGAGGC | | TGAGGCATAAGAATCGTTTGAACCC | TCGGCTCACTCCAACCTCTGCCTCGGGGTTCAAACGATTCTTATGCCTCA |
| 430 | 1013 | GTGGTTGATCTTAGAGTATATTCCATGTG | | ACACTTAAGCAAATGGACCTAATAAACA | P | AAAGAATGTGTATGTTGTGGTTGTT | AAAGAATGTGTATGTTGTGGTTGTTCGGTAGAATGTTCAGTAGATGTTTAT |
| 431 | 1014 | AACATTTTCCAGCATAAACTCTTTTC | | CAGAACAGACAAGGTTGGGTG | P | ATCACCTCATCTCACCTTCCTCTAA | ATCACCTCATCTCACCTTCCTCTAACCACTCAGGATTCATGTCAGCCTAGT |
| 432 | 1015 | TCTGACTCCTCACCTCTTCTGC | | CAAAGACCCTGGGGTGGG | P | CATTTTCCAAACATGCCTTCTTCCA | CATTTTCCAAACATGCCTTCTTCCAGCTATTAAATACTTGAATGTACCGGG |
| 433 | 1016 | TCCTAAGTCCCTCAGCAGAAAAA | P | TCCTTAGTTTACAATATTTACCATTAGTGTCTG | | GTAAGCAATTTGACTTSTATACAGA | TTTGAAAACTGACTCTGGTGTGTACCTCTGTATASAAGTCAAATTGCTTAC |
| 434 | 1017 | TTTGAAACTGGATAATAGGCAGAGG | | GACTTCACTGCCCATGTTACTATCA | P | TTGAAACTTCCTAGAAACTTGTTGA | TTGAAACTTCCTAGAAACTTGTTGAGTGGTTGTGACCAAAATACTGATAGT |
| 435 | 1018 | ATGCACCTCCACTGAGCTG | | CAGCCACTACCTGCATGGG | P | GAGXAGGACAGTGGCTTCTGTACTGCT | GAAGGACAGTGGCTTCTGTACTGCTAACAGACCCCATGCAGGTAGTGGCTG |
| 436 | 1019 | CCTGTTTTTCTGTGGCTAGTGAG | P | GTTTATCTGTCTAGTGACCTTGCAGC | | CACAGCTAGGGAAACAGGXTCTTCACA | CTTATCTCTCCTCCTTTCCCAGGCACTGTGAAGATCCTGTTTCCCTAGCTG |
| 437 | 1020 | ACTGGACACACTACAGATTTCAACAA | | CTTTTAGCAGCTACATGCAAAGAAC | P | CCCAAAGGTCTTTGGCAGTCCGTCT | CCCAAAGGTCTTTGGCAGTCCGTCTGCTTTCTTTAGGGCCTGGAAGTTCTT |
| 438 | 1021 | AATGGTGGCTCATAATAGAAACTAAATTT | P | AGCTCATTTTGGGAGTATGTATGTACA | | TATXTGTAACAGATTCCAACCACAGAG | TGCCACTTCTTTTGCACATTTGAGTGCTCTGTGGTTGGAATCTGTTACACA |
| 439 | 1022 | AGACACACAGACCAATAGAACAGAATAG | | TTATTGAAGAGGCTGTCTTTTCTGC | P | CTCAGAAAAAAATCCACACACCTAC | CTCAGAAAAAAATCCACACACCTACAGTGAACTCTTTTGACAAAGGTGCCA |
| 440 | 1023 | GGTACCGGGGATCTCTGC | | TTGCTTTGGAAAGTATGGCC | P | CACATGGAAAAACACTTTATACTAC | CACATGGAAAAACACTTTATACTACGGATCAGAAGAATCAATATTGTTGAA |
| 441 | 1024 | GCAATTCTCTTTCTATGACAAGGTCA | | TGCCAGGAAATTAAAATCAAGTTAGA | P | TTTCAGCCTCTGATTCCTTTATTAT | TTTCAGCCTCTGATTCCTTTATTATCACAATTTTCTACTCCTGCTCTAACT |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 442 | 1025 | CACTGGCCTGTGAGCCAT | P | ACCAAATGGCAACAACTACTCTG | | ATTGTCTTTTAAGAGAAATCAAATA | TATAGATCAAAGAATTCACTAGAGCGTATTTGATTTCTCTTAAAAGACAAT |
| 443 | 1026 | ACTATGCATCCTGTGAACCCTG | P | GTATCTTTATAGCAATGCCCCACC | | TAGATAAACACCTGAGATAGGGTAA | CCCATTAAACCTCTATCATTTATAAGTTACCCTATCTCAGGTGTTTATCTA |
| 444 | 1027 | ATGTCTGAGAAGGTAGGATCTGGC | P | CAGATACTCATACCTGTACTAGATTCCTCC | | AAAGACTCAGATCCTCATACCAGGG | TCCATGTCTGAGGACGTAGAATCTGGCCCTGGTATGAGGATCTGAGTCTTT |
| 445 | 1028 | GACCAGTGAAATGCAAGTCTCAG | | AGTAAAGGCTGAAAAAGAAGACTTTAATG | P | GAAAGTTTTCATTTCTATCCCTGAT | GAAAGTTTTCATTTCTATCCCTGATGCTGATCCATGCATCCATTAAAGTCT |
| 446 | 1029 | ATCCTTGCCTAAGCATCTGTGT | P | GAAAAATGGACAGAAAKGAAGCTATT | | TTCGTCTTAAGACAGXACACACACAGA | TGCATGTGTGAGTGTGTGTAGGTGCGTCTGTGTGTGTACTGTCTTAAGACG |
| 447 | 1030 | ATTTTTTTTTGTATTTTTAGTAGAGACGGG | P | GGCTCACGCCTGTAATCC | | CAGCACTTTGGGAGGTCAAGGCGGG | TCTCGATCTCCTGACCKCGTGATCCGCCCGCCTTGACCTCCCAAAGTGCTG |
| 448 | 1032 | CTGGTATTCCCTTCATGAGAATTTT | | AGGACAGTAGGAATGTTGGAATAGAC | P | AATGCCTTGGTAAAGACAGTTTTCT | AATGCCTTGGTAAAGACAGTTTTCTCCAAACTCCCTGAGAGGTAGGTCTAT |
| 449 | 1033 | TGGTTTCCTGTGTGGTAGTTCTTT | | GAAAAAGAAGAATTAGATTGGCACC | P | TTCCGTCATCTGTTTATGTTATTCC | TTCCGTCATCTGTTTATGTTATTCCGCACTCTTTYAGTTTTCAGAGCAGCA |
| 450 | 1034 | GTTCCCAAGGGTACTGGGTG | P | AGGGTACATGGAGACCTGGG | | AGCTGAATTAGTATAXCTTACAAGTAT | AAAGGGAGAGAGTCTTTATAATTTACATACTTGTAAGCTATACTAATTCAG |
| 451 | 1035 | TTTTGTGTGTGTGTGTGTGTGTG | | GAGACCTTTTATGTTTTGCTCTAACCT | P | TGTGCCTGATCTCTTGTGTTTTGAG | TGTGCCTGATCTCTTGTGTTTTGAGGTCCTAGTGAGGAAATGAGGTTAGAG |
| 452 | 1036 | TGTAATGGTCATGGACAGTGATG | | GACTTCACCACGAGGGCA | P | TGGGAAGTAGTGAGTGATGGTGGGG | TGGGAAGTAGTGAGTGATGGTGGGGAGCCTAGACCTCAGGTCATGGAGCCA |
| 453 | 1037 | TGCTCAGTAAGACCCCAAATTTT | P | ATATAGTCGTTATAACAACAGCTTCAAAGTC | | CAGCTTCAAAGTCAAATAGACAATG | TCCCRTGGCAGAACTTTGATTGAACCCATTGTCTATTTGACTTTGAAGCTG |
| 454 | 1038 | ACCCAATTCATACCAAATACTCTTCTG | P | ATAACAACAGCTTCAAAGTCAAATAGACA | | AATGRGTTCAATCAAAGTTCTGCCA | AAGACCCCAAATTTTGTCTAATCCCGTGGCAGAACTTTGATTGAACYCATT |
| 455 | 1039 | CAGGGCAGAAAATCATAACAATG | | AAAAATGCCTCCAACCTTTACAC | P | TTCTTCCTAGGGCTGAATAACCAGA | TTCTTCCTAGGGCTGAATAACCAGAGTGATTTAAGAGCTAGGGAATGTGTA |
| 456 | 1040 | CTCATCAAAAAGTGGGCTAAAGATAT | | ACGGCCATTCTTGCAGAA | P | GAAGGTATACAAATGACAAAAAAGT | GAAGGTATACAAATGACAAAAAAGTCATGGAAAAATACTGAATATCACTAA |
| 457 | 1041 | CAATGTAAGAGTTTCTACTCTCATTTTTCTG | P | CTGAAGACCCCATCATAGTCTTTG | | TTXTCTCAGCATTXCAGGGGGTGAAAG | TTTAGGGCTCAATGCTAGCCATCATGCTTTCACCCCCTGAAATGCTGAGAA |
| 458 | 1042 | CTCACCACTGCACTCCAGC | P | CACTACCAGTTTCTTATGTATCCTTCTAAAG | | TCCTATACTTAAGAATACAAATATA | TGTGTATTATTTATATGTAATTTCTGTATATTTGTATTCTTAAGTATAGGA |
| 459 | 1043 | CCTTTTGATGTTTGGGGTTTTC | P | TGTTCAAGGACAAGGTATCCAAA | | AACAGCCTXGACTTAXTTCAATGAGAC | TTTTCCCTGAACTGAACTGATATTCCGTCTCATTGAATTAAGTCAAGCCTG |
| 460 | 1044 | GAACTTCAACATGATAATAAAATTCACCA | | TGGGAATTCATTTGGCTTCC | P | ATAAACXTAACTGAATAAGAGCAATAA | AAACTTAACTGAATAAGAGCAATAACAATTTTTAAAAAGCTTAAAAATGTA |
| 461 | 1046 | CCAACTATAAACTTTACCTATGGAAAAATG | | TGGAGCACTTTAAAAATATTATCTCACTG | P | AGTGTTGGGCCATTAXATGXTCTCTTA | TGTTGGGCCATTAGATGATCTCTTAGTGCTCACCTATTTTGAGACTTCAGT |
| 462 | 1047 | AGGCAGAATCAAAGGCTTCT | P | CGGCATGTAAATAACTTTTTAGGGA | | AACGGGCCATACTAACAAGTGCTGC | GGATCTTTCCAGGCAGAATCAAAGGCTTCTCGCAGCACTTGTTAGT |
| 463 | 1048 | CATTAAGCCTTTCACTGAGAGTAGAGAT | | AGCTGGAAGGGTTTTGAAAGAT | P | ACTTGCAGTTGCCTCTCTGACACAA | ACTTGCAGTTGCCTCTCTGACACAAGTATATCTAAGAAATCAACATAATCT |
| 464 | 1049 | TTCAATAATGAGAGGGGAGAAG | | CTCTCAGCTTTTTTTCTTGCTACTTG | P | TGGXAGGXAGTGGGCTTCATATTCATT | GAAGGAAGTGGGCTTCATATTCATTCGCACAGCTCCTCTCAACCTGGCCCC |
| 465 | 1050 | CGAAATGGCAATTTGTCTGAA | P | CATATACACAGGTATTGTTTCCAAAGC | | AACATACTCTGCCCATTCCAGCCTT | ACCAGCACTTAGGTTATCATATTGGAAAGGCTGGAATGGGCAGAGTATGTT |
| 466 | 1051 | TTGCTGTTTTTGAGCTCTATATTACATAAA | | GGCATTAGAAATTGGAGTAAAGGC | P | TTGAGCATAAACAAAATCCAAACAA | TTGAGCATAAACAAAATCCAAACAAGTTTTTTGCCAGTTGATAACATGGAT |
| 467 | 1052 | CTTCTTTGGCTATCATTTGGACAT | | TGGTATGAGTGTGTGTTKGTGTTTTA | P | CCATTTCAAACATAATAGTCAAAGA | CCATTTCAAACATAATAGTCAAAGAGAAGAAAATGCTCTATTCATTAAAAC |
| 468 | 1053 | GTATCAAAAGTGTCAATTCCCAAAGA | P | ACACACACACACACACACACAATC | | CTACCTTTWTAATCTAXATTGACCCAC | TATGGGATTAGCATCTAAGTGTCCTCGTGGGTCAATATAGATTAWAAAGGT |
| 469 | 1054 | AAGGTATCTTCTTGGCTCCAGTAAA | | CCAAGGTCACAAGCTAGTCTTAGC | P | AGCACCAGGGCTAGGAGTTCAGAGA | AGCACCAGGGCTAGGAGTTCAGAGACGTGGCATTTCATACTGGCTAAAGCT |
| 470 | 1055 | TTTGGAAGGCTCAGAAAAATACAG | P | CAAAGACATTCAGCAAGTCTCTAGAAA | | GTCTTCAAAGCCCTCCAAGTCTCTA | AAAATGTGGGAAAGTTTGGAACTTCCTAGAGACTTGGAGGGCTTTGAAGAC |
| 471 | 1056 | TATGACCAGTGCCTGTCTTAACTG | P | TATTTGAAGAACAGAAAAGTCTAGTGAAGC | | TGAAGCCAGACAGCAGTAATCAGGA | CCAGCTTCAGTGTGCACCAAACTCACTCCTGATTACTGCTGTCTGGCTTCA |
| 472 | 1057 | AGCTACTAAGAGTGCTGTGACTTTAAACT | P | CCATGCAGTTAAAAAGAAACTCG | | TCGCCAGAGACTCACATCCTACCCA | AAAATAAGTGGCAAACCAGTGGTTTGTGGGTAGGATGTGAGTCTCTGGCGA |
| 473 | 1058 | AGGCAAGGCTGAGTGCGC | | GAAAAAGAACCCTTAAGAAAAGATGC | P | AAAATGAGCTTGTTCCCCTGAGGAG | AAAATGAGCTTGTTCCCCTGAGGAGGTGTGACATCGCTGTCCACCCATCAC |
| 474 | 1059 | CTTTGGCTGTGTACTGATTTACACATAT | P | CATTTTAACTGTTGGAATCACAAACA | | GCTCTTTAGCCTACTXCTTTCCAGCAG | AAAAGTACCCAAGGCCGGGGGGGAAACTGCTGGAAAGCAGTAGGCTAAAGA |
| 475 | 1060 | GGAACTTGATATGTCTGAAAGCAAA | P | TTCCGAATTTCTTTGGAAGATGT | | GATGTTACTGGTTGATTTCCATTTG | AAGTGGAAAGTCTTTCAGAATAATGGCAAATGGAAATCAACCAGTAACATC |
| 476 | 1062 | TTGTTGAATGGTTGTAACCAAAATG | P | CTTTGCTAAAGCATACCAAGAGTGA | | TACTCCAGTTCCCAACAAGTTCTGC | AGGCTGAGGTGGTCTCAGCTGGAGACGCAGAACTTGTTGGGAACTGGAGTA |
| 477 | 1064 | CTAAGGCACTGGTTCATTACTACATAATG | | TCTCAACAAAAGGCTTTGATATGG | P | GGAATAGTTGAGCTAACCAATTCAGAGG | AATAGTTGAGCTAACCAATTCAGAGGCATTCTCTAGAATATAGTTAAATTT |
| 478 | 1065 | TGTGGCTCCCCTGAGTATTC | P | GCTCAACTATTCCAATTTACTCATTATGTAG | | TAGTAATGAACCAGTGCCTTAGATT | GAAAATTGTGGGCAGATATGGTGGTGAATCTAAGGCACTGGTTCATTACTA |
| 479 | 1066 | TATGTCAGGCCCTAGTATGTAGTATGAGT | P | TATGAATCTGAAATCCCCATCATC | | AGGATATAAGCTCTCTGAGGGCAGG | CAGTGGTGAACAGGACAGATATAGCCCCTGCCCTCAGAGAGCTTATATCCT |
| 480 | 1067 | RGGCATGGTGGCAGACAT | P | CTCATTGTAGCCTCCGCCT | | CCTGGGTTCAAATGATTCTCCTGCC | ATAATCCCAGCTACTCAAGAGGCTGAGGCAGGAGAATCATTTGAACCCAGG |
| 481 | 1068 | CACAGAGTTCCCCTCCCC | | GTTTCAACTTACAGGAAAATGAGGG | P | GCTCTGTAATCTTGTCTGCGGAGGC | GCTCTGTAATCTTGTCTGCGGAGGCGATTCCAGGCTTNGCTGGACGGCCCC |
| 482 | 1069 | TGCTCCTGCTTGAGCCAG | | GTAACCGCAGATCTTGGAGG | P | CTTTCCCAATATAGACAGACGAGAG | CTTTCCCAATATAGACAGACGAGAGGTGAGCAGGGTCTGCTTGATGAAATT |
| 483 | 1070 | CCAGGCTGGTCTCGAACTTAC | | ATAAAATAATTTTTAAAGGTCTGTTTAGGGC | P | TCAGCCTCCTGAAGTGTTXGGATTCCA | AGCCTCCTGAAGTGTTGGGATTCCAGGTGTGAGCCACCACACCCAGCCCTA |
| 484 | 1071 | TTTGGTTTCTCTCCGGTTGG | | GAATATTTTTCTTCTTGGGAGAGGC | P | CXTGAAAATATCAGATCCCTCATGAAACGTGGCCATGGCTATATTTGCTACACT | TGAAATATCAGATCCCTCATGAAACGTGGCCATGGCTATATTTGCTACACT |
| 485 | 1072 | CAGGGGTCTGTGAGGTCAGA | P | ACAAGAATATGTAAATACTCATTTCATTAGTCAC | | TCATTTCATTAGTXACAAAAGTGAT | GAGACTACACGCCATGTAATCGCATCATCACTTTTGTGACTAATGAAATGA |
| 486 | 1073 | AAGACCCTGACTCTAAAAAGCAAAC | P | CTATGTAAGGGTTAAGGTGGCTAGTCT | | GATTCGGTACAGGTTTTACXGCTCTGT | CTGAAAAATGTGATTGGTACCAAGAAACAGAGCTGTAAAACCTGTACCGAA |
| 487 | 1074 | GTGGTTCATGCTATACCAAGTCATT | P | TGAGAATTTGTAACACTTTTTGCTTAGTC | | AAGTTTTATTTTTGCCTTTGTTTCA | GGTCAGCATATAGAACTTATTTTGCATGAAACAAAGGCAAAAATAAAACTT |
| 488 | 1075 | CTGCTGTTAGTCTAATGGGATTCC | P | TCCAATTTTCCAAGGCTGAA | | TGAAATAAAAGAAAGTATGXTAAAGGC | TAGGTAACCTGCCCTTTCTCTCTAGCGCCTTTAACATACTTTCTTTTATTT |
| 489 | 1076 | CCAACTTGTTTGCTTTCTCCC | | TGGTTCTCAAATAAGACAGACAAAAA | P | TAAATTTXGCCTCTTTACAATCCCA | TAAATTTGGCCTCTTTACAATCCCACATTTCTCAAAGGTTTTGTTTCTTTT |
| 490 | 1077 | AGTCTACTGTTTATTTGAGAAATGGCTT | P | TAGTTATTTTCTTACCACTAAGGTTATAGGGATAT | | ACTAAGGTTATAGGGAXATGAAAGAAT | ATGTGTATTTAGCTAAGAGTTTCTCCATTCTTTCATATCCCTATAACCTTA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 491 | 1078 | GTTTCTGGMACTTAATGATTTTTCAAA | P | AGCATAAGGATGGCATAGGATTC | | GATTCAAGGATTTTTTTTTCTGTAA | TTAGTTTCTTCTTGGATATTAACAGCTTACAGAAAAAAAAATCCTTGAATC |
| 492 | 1079 | TGGTGACTCACGTCTGCAAT | P | CTGACTAATTTTTGTATTTTTAGTAGAGAATGG | | TCGAACTCCTGACCTCAAGTGATTC | CAACACTTTGGGAGGCCTAGGTGGCGAATCACTTGAGGTCAGGAGTTCGA |
| 493 | 1080 | AAAAACAACAGCAGCTCCACA | P | GAAAGATAAGGAAACTCAGCTTTGG | | GAACATTGCAGATCACACAACCCAC | TTCCCAATGCTCTTGAACAGGTCCTGGTGGGTTGTGTGATCTGCAATGTTC |
| 494 | 1081 | CTTGCTAGAAACTTGTTAAAYGGTTGT | | AGTTCCTTATTTCCACCTGAGACC | P | GATCAAAATGCTGATAGTGXTATGGAC | TCAAAATGCTGATAGTGATATGGACAATGAAGTTCAGGATGAGGAGGTCTC |
| 495 | 1082 | TGAATACAACACACACAATGGAC | | CTTAGACCGGCCTGGAG | P | TTCCACACCAGCGAAAGAGGGAGACGCAGACAGGCCGCACCGGGCCTCCGA | |
| 496 | 1083 | CTATCATGCAGTGAGATATATGGTTGTAA | | TCTAGACAAGTGTAATTATAGAAAGAAAGTGAAA | P | CTTGGTATACTGCATCTCTXAAAATGG | TGGTATACTGCATCTCTTAAAATGGGGGTTATTTGTATATGACTAAATAAC |
| 497 | 1085 | GAGAGGCACTAAACAGACACTTAAATT | P | TCTTTAAGCCTCCAGCAGTGC | | AGAXATTTAATTGATTTTTTTTATTTA | AATAAAAACCTCAACTTTTAGAAGATAAATAAAAAAAAATCAATTAAATTT |
| 498 | 1086 | GGACATGGCATATCTTTTCATTTTT | | AGCACAGAAAATTAACTACTTAGGAAAAAA | P | AGTTCTCTTCAATTTTCTTCATCAG | AGTTCTCTTCAATTTTCTTCATCAGAGTTTTATAGTTTTTTTTGTAGAGAT |
| 499 | 1087 | ATTTGTATTTCAGATCCATCTAGACTCCT | | GGAGAGACTACGTGAGGGTGG | P | TCTCTTCCTGGTGACCXTGTTGCTTCC | TCTTCCTGGTGACCATGTTGCTTCCCCTCTCTAGGGTTTTCCCAGCCCCCA |
| 500 | 1088 | TGCAGTCCCAGCTACTTGG | | CTTGGAGTACAGTGACATGATTATGG | P | GTGGAXGTGGGAGAATGATGTAAGCCT | GGAGGTGGGAGAATGATGTAAGCCTAGGAGGTCGAGGCTGCAGTGAGCCAT |
| 501 | 1089 | GCATTCTCCGAGTTTGATTATGTT | | AAAATTCACAGTTTAGGCCAGTCA | P | ATGAGAAAAAAAGTGTTXGACTCTACA | GAGAAAAAAAGTGTTAGACTCTACAGGCATAAATATTGAAAAAACTGACTG |
| 502 | 1090 | TTCCCTGTACCCCACCCC | P | CATAAAGCAGAATGTGGTGTGTG | | GCTCACTGGXAAAGATXCTTGGAACAT | TGCTCAACATGTTCACACAATTCTCCATGTTCCAAGGATCTTTCCCAGTGA |
| 503 | 1091 | CAGCATTCGGTGAGAGCAA | | TAAAAGTTTGGAGCAAATAACCCA | P | CAAAAGTAGCTGTCGGCTGAACACA | CAAAAGTAGCTGTCGGCTGAACACAGGAGTTCATGTGTACTTTGTGACTGA |
| 504 | 1092 | CCTGTTTCTGGGCTCGACA | | TTTTTGCTCCTATTGTATATGTAGAAACTG | P | TGTATCACCCCTAACAAGTCATTTT | TGTATCACCCCTAACAAGTCATTTTGCCCATTGGAACTTCAGTTTCTACAT |
| 505 | 1093 | CGGTACCCGAGAGGATCTG | | TTCTTTGCTTTTTGTAGTGTAGGAAACTA | P | CAAATCXCTGCTGTTTCTAAGTGAACC | AATCACTGCTGTTTCTAAGTGAACCGTTATACTTAGTTTTATGTAGTTTCC |
| 506 | 1094 | TTYATAATAAGAAGGCCCTGGGT | | CTTGCTACCAGCTTGAGGCT | P | CTGCTTCTCTGGGATTCTCTCATTC | CTGCTTCTCTGGGATTCTCTCATTCGTACCTCTCTGTTCATGATGCTGCAG |
| 507 | 1095 | TAGTTCCAGCAGGGGCTAGAA | P | CTCTTTAAGTGTCCTCCCTGGG | | TXTCCCTCTGAATTAGAAAXCTCTAGT | ACCAGAAACCAGTTCATCAAGCTAAGACTAGAGCTTTCTAATTCAGAGGGA |
| 508 | 1096 | CAACCAGAGGATTCAACAGAGTT | P | CAGCGTGGTGCTTCATGA | | CCTGGCCACTCTCGCAGAATAGTCA | AAGGAGCCTGACGGTTTCACAGAGTCTGACTATTCTGCGAGAGTGGCCAGG |
| 509 | 1097 | CTTTCTGATTGTTACACTTTTTTTTTCC | | CAGGGGAATTGCTTGGACC | P | CXAGGCTGGGGTGXAGTGGTGCGATCT | AGGCTGGGGTGCAGTGGTGCGATCTCGGCTCACTGCAACCTCTACCTCCCG |
| 510 | 1098 | TACCGGGGATCTTATCAATAGTGA | P | CATGAGACCTGCCAGGAAAA | | CTTTGGTCTGACCTGAGAGXTCATACC | GAGTCCAGCTCCAGGTTGAAGTCCTGGGTATGATCTCTCAGGTCAGACCAA |
| 511 | 1099 | TCAGGTCAGACCAAAGGCA | P | CTTGAATCCTTGACTGCACCTC | | ACACTACGATGTGGGGAGGACAACT | TTTTCCTGGCAGGTCTCATGGGAGAGAGTTGTCCTCCCCACATCGTAGTGT |
| 512 | 1100 | CTTGTGAGTTCAATTTTTTTCTCTCTC | P | TTTTATCCTGGGTTTCTAAATTATTGC | | TAAATTATTGCXGTAAACTGATTACAT | CTTCAAAGAAGAGCCCATATGGGAAGATGTAATCAGTTTACTGCAATAATT |
| 513 | 1101 | ATTAGAAACATCCTTCCCAGGC | P | GTTTTGTTCACTTGTCTCAGAACATG | | GAAAACCAAGGGAGAGAACAAACTC | GGACTATCATCATCCTGCTCCCTCTCGAGTTTGTTCTCTCCCTTGGTTTTC |
| 514 | 1102 | GGCATCCCAGAAGACATCTC | P | TTTTATTCCTAGAAAATCCTCCTTTCC | | TCCTCCTTTCCTTCTAXCACTCTGATC | AGAAGATAGCGTTAACATATCTAAAAGATCAGAGTGATAGAAGGAAAGGAG |
| 515 | 1103 | CGGGGATCTTTTCCTTGTATTA | P | GTTGTTAGACTCGTGGGACGAC | | CACTGTTTAAGGGTAGTTGTGGTGG | TTTGATAGCCTSTGACACTAAGATGGCCACCACAACTACCCTTAAACAGTG |
| 516 | 1104 | TGCCTCAGCCACCCAAAG | | TTCAGTTCACTTGCCCACTTTT | P | TGCTGXGATTATAGXCACGAGCCACCC | CTGGGATTATAGGCACGAGCCACCCGTGCACAACCAACAATTCATTTAAAA |
| 517 | 1105 | AACGTGGAAAGGACCACAGC | | CTTCCACACAGGTGTACCCAC | P | AGGACACCTGAGCTCTCCAACAGAC | AGGACACCTGAGCTCTCCAACAGACGTTTAACGCCAAGGGATTCACAGGTG |
| 518 | 1106 | CTAGCATTTCTCTGAAGGATAAAACAAA | P | AGGGYCAATGGAGATTGCA | | TTTTAATTCATTGAAGTTATTTTGG | CAAACAAACAAATTAACAAGAAAAAACCAAAATAACTTCAATGAATTAAAA |
| 519 | 1107 | AATCTACAGCATCAGAAAGACTTGTCTC | P | CTACTTCTCGCCTCCYAAAGTGCT | | AGTXCTGGGATTACAGGGATGAGGCAC | AATAATCAGAGCTCTGGCCAGGCGCGGTGCCTCATCCCTGTAATCCCAGCA |
| 520 | 1108 | CTAGAGTTGTTTCAAAGCTAAAAATGGT | | TTTCTCTCAGTTTGTAGGCTCAAAA | P | TCCATACGGGGCTAAGTGAAATAAG | TCCATACGGGGCTAAGTGAAATAAGGTTCCACCTAACAATCTCTAGTTTTG |
| 521 | 1109 | GGTTGTGTGTTTCTAAGGATTTGG | P | ACCAGAATAATTCTAACCAGAAAGGAA | | AGAAAGGAAAAAGACGCATTAAAAC | TAATACATTTTTAAAAAATAGAATCCGTTTTAATGCCTCTTTTTCCTTTCT |
| 522 | 1110 | CTGACACATAAAGAGTCCACACATTT | P | TTGTTGTCCTGGTTTTCAATAATTT | | ATAATTTGGTTCTATTTTCTAACAT | AGCATGCAACAAAAAAATTACCAGGCATGTTAGAAAATAGAACCAAATTAT |
| 523 | 1111 | CCTTTCACAACACGAGGGG | P | AAGAGATAAATAGGAATGTGTATGGGAA | | GTATGGGAAATTGTGAAGTAAAAGG | AAACCATATCACATTTTTAAAAATTGCCTTTTACTTCACAATTTCCCATAC |
| 524 | 1112 | ACACGTTGGAATTATGGGAGC | | CATGTGGTCTTGAAGGGGTCT | P | GTAAGATTXGGATGGGGACACAGCCAA | AAGATTTGGATGGGGACACAGCCAAACCATATCACCTCCATTGAGCTTACT |
| 525 | 1113 | ATTCCCCAGCCATGCTAAAC | P | TACATTCCAGCCTGGGCA | | AAAAAATAAAAGTAAAGACATACCC | CTTTCCTTTATAAATTACCCAGTCTCGGGTATGTCTTTACTTTTATTTTTT |
| 526 | 1114 | GTGGGGCTCAATACTCATGCT | P | TGTGACTAAGTAAAAAACATTGAGATTATCC | | AGATTATCXTGATTTATCXTTATAGGT | TTCAAGAGCTTTTATGATCACATTACACCTATAAGGATAAATCAGGATAAT |
| 527 | 1115 | GAGCTATCTATGACAAACCCACAGA | | TGGTGAGAGTGGGCATCC | P | CATCATAACGAATAAAATCTGGAAG | CATCATAACGAATAAAATCTGGAAGGATTATACTTGATAACTATAATAAGA |
| 528 | 1116 | GAAGAGGCATTCTATTTCAGCAAG | P | TGCAGCATAAAAGCAAGAGGG | | AGTGGCAGGAGAAAAACTCAGGTTA | GGTTTTCAGAAAAAAAAAAAAATAAGTAACCTGAGTTTTTCTCCTGCCACT |
| 529 | 1117 | CATTTGTTAAGTCTCTTTACAAGGCC | P | TGGGCAAGGACACAGATG | | GCAXACCATACCATGATGTTTACTTTT | TGTTCCTTTCAKAGTCAGCAAATAAGAAAAGTAAACATCATGGTATGGTTT |
| 530 | 1118 | GTGGACATTCAGTACATTTGTTAAGTCTC | P | ATGCAAACCATACCATGATGTTTAC | | TGTTTACTTTTMTTATTTGCTGACT | TTACAAGGCCCATGTGTTCCTTTCAGAGTCAGCAAATAAKAAAAGTAAACA |
| 531 | 1119 | GTCTCTCTTTCTGAAAATCATAGAAGGAT | | TGCAGAACATTCTTTTTTTGGC | P | AAAAGTTCCAAGTCAAACACATTCA | AAAAGTTCCAAGTCAAACACATTCAGCTTTCATCCTTTAAAAATGTCATTA |
| 532 | 1121 | CATCTTTTTCTAGTTGTGGCTTATCTTT | | TGGGGAAAGTGATGAGGATTT | P | TCACACAATTXAAGCTGATATTTAAGA | ACACAATTTAAGCTGATATTTAAGAAACAAATTCTTAATTTAAATAAGATT |
| 533 | 1123 | AGGTGAATGGGAAGCAGACATAT | | GTACCGGGGATCTGGTTGTT | P | GGTGGATCAGGAGAGAGAGAGTGGA | GGTGGATCAGGAGAGAGAGAGTGGAGGGGGAAGTGCTACACACCTTTTAAA |
| 534 | 1125 | GCAACAAACTTGCCAGCTC | P | GCTGCTATAACAAAATATCTGAGACTGG | | AAAXAACAGAAATGTACTTCTCACAGT | TTGATCTTGGACTTTCAGCCTCCAGAACTGTGAGAAGTACATTTCTGTTCT |
| 535 | 1126 | AATTCAAGATGAGAATTGGGTGG | | GAATTRAAAATGAGACAGCCAGC | P | GATGAAGCTTAGGTGACAGATTTTG | GATGAAGCTTAGGTGACAGATTTTGAACATGAGACCAATCCACCCACAGAG |
| 536 | 1127 | CACAGGCAAGTAATTCATTTTGTG | P | ACAGTTTTCAAGGTTATAAATGACTGTCTT | | ACTGTCTTCCAAAAAAAXCTGATGACA | TATTTCTTGAATGGGGCAGAAAGTTATGTCATCAGCTTTTTTTGGAAGACA |
| 537 | 1128 | TCCTAGATGACCCCTGGCTT | | CGGGGATCTGCTCGGGTT | P | GGCTGGTGAGCCTGGGGACTTGGTG | GGCTGGTGAGCCTGGGGACTTGGTGGGAACTTCTCTGAGAAAGGGAAGCAG |
| 538 | 1129 | CCCGTATGGAATTTCAGACTACTTT | P | ACAAGTGATGGTTAACTACTAAAAACTGAATAA | | CTAAAAACTGAATAAGCATCTCCGC | TTTGCCTCTGGGTCTTTCACTGAAACGCGGAGATGCTTATTCAGTTTTTAG |
| 539 | 1130 | TGTGTGTGTATGTGTGTGTTGG | | CAAGAACACCTGCCCCGT | P | AGAGTTATTGAGAXAGCCAGACTTTTT | AGTTATTGAGAAAGCCAGACTTTTTAAAAAAAAATGCAAATTTCCAGGCCT |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| | | | - | | - | | |
| 540 | 1131 | ATTAAGATGCAGTGGGAAGAGCT | | TTATTGTCTATCCTTCTCTCCATAAAATAAAG | P | TTTAGAGTXCCXGCTGTGTXCCAGGCA | TAGAGTGCCTGCTGTGTGCCAGGCAGTTTCTAGATGCAGTAGGTATACGTC |
| 541 | 1132 | AACATTGGTGCACTGGTACCC | | ATGATCTTTCTAATGCTTTCCATGAA | P | AAAGACTTAGACAGCCACACAATAA | AAAGACTTAGACAGCCACACAATAACAGTGGGAAACTTTAACACTTCATGG |
| 542 | 1133 | GTAGGAGTCCTTTCATTTTATTCTTCTTTT | | TGCCATTTCTCCCCCAAA | P | CAATTTCTACAAAAAAACCATCTTG | CAATTTCTACAAAAAAACCATCTTGGATTTTAATTTTGATTTCAATTAAAT |
| 543 | 1134 | GTTCATACTTAGCATAGTAGMTGATAGGTAAT | | TGGAGGTAGGTCTCTATGACATGC | P | TTTAATAAATTGGTCTTCTACCCTT | TTTAATAAATTGGTCTTCTACCCTTGTTTCATTCCTCTGGCTTCTATGATG |
| 544 | 1135 | CCACTTCACACTTTTTGGTATTTTTT | P | AGTTGCTAGGTTTGGGATACTTTTAAA | | AAATACAGCAATAGATACCAAATAT | TCACTCCACTGATGGTACCAAAACCGATATTTGGTATCTATTGCTGTATTT |
| 545 | 1136 | ATTTTTGCACTGGTTATTTCTCTCTG | P | CAYTGGGTAAATACAACCATTTCAA | | AGAAATTGGXCATAACAAAGAGGCTAC | CTGGATTTCGGATTTGCATGGGCCCCGTAGCCTCTTTGTTATGGCCAATTT |
| 546 | 1137 | GATTGCTTGAGGCCAGGAG | P | ATAATAAACCACCCAGTATAACCACATATTTA | | CATATTTAGTCCTXTTCATTAAAACAA | TTAGAAAAACCTATCTCATCAATTCGTTGTTTTAATGAAAAGGACTAAATA |
| 547 | 1138 | ATCTCCACACCACTCTCCTGATC | | GAAAGATGTGACAGAAAATACTGATTAGG | P | GGAXTGCATGTACACAGTTTGATGGAC | ACTGCATGTACACAGTTTGATGGACGTCTGTGTGTGGCTGCCTCATACAGA |
| 548 | 1139 | GATTTGAGTGATGAGATATAAGTTATTTTAAGATG | P | TCATTAGTGCTTAAGTTTTGAAATTGTG | | AAGCATATTGGATTGGXTACTTTAGCA | TTTCTAGGTAAGAAGAAGAAAAATTGTGCTAAAGTAGCCAATCCAATATGC |
| 549 | 1140 | CGGGGATCTGAAAAGCCA | P | TAAATGTGTGGTGAACCACGG | | TTTTCAGTACAXAGACAGTCCTTTAAC | GCTTGAGTATCTGCCAAGTTTTTAACGTTAAAGGACTGTCTTTGTACTGAA |
| 550 | 1141 | TAATCGTTAGCAYCTTCCAGAATTC | P | CTCTACTACAGGGAGGCTCACAAG | | ACAAGATAAATTGXCTCCCTTTGGCTG | TGTTTGTGTAATTGAAGAAAACAACACAGCCAAAGGGAGGCAATTTATCTT |
| 551 | 1142 | GACTCTGAGCTTGAAGAACCTCC | | CTTCAATTACACAAACAGCAGCC | P | TGATAATXCAAGTXCTXATCGTTAGCA | ATAATGCAAGTGCTAATCGTTAGCACCTTCCAGAATTCTTGTAGTTCTCAT |
| 552 | 1143 | CCGTATGGAATTTCCTAAAAGTATAGAAA | | TGCCGACATAATGCTGGG | P | CCTCATGATCTGCTAACTCCACTTC | CCTCATGATCTGCTAACTCCACTTCCCGAAATAAAATCAGTATTTTCCAGA |
| 553 | 1144 | CATTTTTTCTGTCTAATCTGCCCTTA | | TAAAAGTGACCCAAATGAGAGTTCA | P | TACCCAGGTTATTTTTTATTTTAGT | TACCCAGGTTATTTTTTATTTTAGTGATTGTAGTTGTCATTGGTTGAACTC |
| 554 | 1145 | GCCAACATCTATTGGGTTTTTTTT | P | CCAGGGAAATGCAAATTAAAATG | | CAGTGAGATACCACCACCTTATTTC | ACTTTTTAATAATGGCCATACTTGCAGAAATAAGGTGGTGGTATCTCACTG |
| 555 | 1146 | AAGCAGGGAAACTCCTTAGCTTT | | CATTCTAAATAGCTACTTTCCAGGGG | P | AGAGGTCCATCTGACTGTTGATTTG | AGAGGTCCATCTGACTGTTGATTTGCGATATTTAGTCTTCCTATTACAGTT |
| 556 | 1148 | ATCTAAGGAGCTCTGTAAATGACTATCC | P | ACGTTGAAGTCAGTACGCAGG | | AGGCTGGCATAGGCXTGATACCTGG | CAAGGTCCTATGTGTTAGTCCTTGCCCCAGGTATCATGCCTATGCCAGCCT |
| 557 | 1149 | AAAAATGTACTGAGCTTCTTGTCACATAT | P | GATGAGTCCAAGGTGGGCA | | CAGXGTCAGATCXTACAGGTCCCCTTA | ATAGAAATCAGGTCCCTTTGCAGGCCTAAGGGGACCTGTAGGATCTGACCC |
| 558 | 1150 | CAGAATATACATTCTTCTCATCTGCACA | | ATAGTTTTGACTGTTCCTCTTTGTGTTC | P | TCAAGTACTTTCTCAGGTCACAGGA | TCAAGTACTTTCTCAGGTCACAGGAGAATAAAACTAGAAATGAACACAAAG |
| 559 | 1151 | AAATGGGCACAAGGATGG | | CTTTCTCATGGATCTTGGACTTCT | P | AGGGCGTTXCACACAGGGCATTGTCTT | GGCGTTGCACACAGGGCATTGTCTTACCAGAGGCAAACACTCTGGGCTGTG |
| 560 | 1152 | GAATGAGTCAGGATATAGCAAGTCTATAATACA | | TGGAATTTGTGAAAATGCTAACTTG | P | TAGCAATTCAAACAGAGGGAAAAAAA | TAGCAATTCAAACAGAGGGAAAAAAACTATAAATTGCAGAAAATCTACRTT |
| 561 | 1153 | TACCGGGGATCTGCTTAGC | P | GAGCTCCCACAATGAWCATGG | | CTACACTGCACTGCTCTXTAAGAAACT | AAGCATTAAGTTTGATTGTTGTGCAGAGTTTCTTATAGAGCAGTGCAGTGT |
| 562 | 1154 | ATCCAGCTATAATCCTCATTGCAC | | GACAACCAAGTATCTCAAAACCCA | P | CTGTGTTGXCCTTCAGCCTGTTAGACT | GTGTTGGCCTTCAGCCTGTTAGACTATTTTACGTAGGACTGAACCAACCCC |
| 563 | 1155 | ATAAGAAGGTGAAGCTGTAGGACCA | | CAAATACAGGGAGATTTTCTAATGATTTT | P | CAAACAAGGGAGAGAAAGGGAGTCC | CAAACAAGGGAGAGAAAGGGAGTCCGAGGAATTGGGGACCTGGCCTAACAA |
| 564 | 1156 | TTATACTCTAATTCCTAAGCATCAGTAACACA | | GGGGATCTGTTGAAGTTCCTCT | P | CTATGAAAGTTAACAGAAGGTAGAA | CTATGAAAGTTAACAGAAGGTAGAACTCAGCTGCCCCTGCTCACAAGCATC |
| 565 | 1157 | ACTGTTGTACCCAGGAAGCATG | P | TAATTATTGCCGTCATCACCCT | | AACTATGTTXAAGGGCTXAAGATTCAC | TGCTGACAGAAAAGAAGTTTCAATACGTGAATCTTCAGCCCTTCAACATAG |
| 566 | 1158 | TGGGTTATAGTCAAATGGTAAGGC | P | GTATTTAGCAATTTCAAAAAGTAGACCCT | | CTCCATCACTGGCTGTTGXAGTCTTCT | AAGCAAAATACCCCAATTCTGAAAGGAGAAGACTTCAACAGCCAGTGATGG |
| 567 | 1159 | TACACTGTGATCTGAGAAGATATTTGA | | CGCTAATAGACATCTACAGAACATTCC | P | ATATTATTXCATTGTTTTGXATTTATT | ATTATTTCATTGTTTTGAATTTATTGAGACTTGCTTTATGGCCAAGTGTTT |
| 568 | 1160 | CACAAAGCATTAGTGACTTTAGTGACG | P | AGTCGTTAATGAGTGATTTTAAATAGCTTG | | TAAATAGCTTGCTGTGTGCTTCCTA | TGAGGATTATTGCCCAGACTTCCTACTAGGAAGCACACAGCAAGCTATTTA |
| 569 | 1161 | CCTACAAAAGCAATGCCCTG | | CCAGCCCCGCTAAACTGT | P | TCTCACACTCCTAATAAAGACATAC | TCTCACACTCCTAATAAAGACATACCCAAGATTGGGTAATTTATAAAGAAA |
| 570 | 1162 | CAAGATTAAAAGAGAAATCGTTGARAATAC | P | CTGCTGCCCTGTGAAGAAGT | | CCATTATGATTGTAAGTTTCCTGAG | TCACAGTTCCACATGGCTGGGGAGGCCTCAGGAAACTTACAATCATAATGG |
| 571 | 1163 | GGATCTTGGGACGCTGTG | | CCAGTAATGGAATTGTTGGCTT | P | GXAAGCTGTXTGGAARTTTCACAAAGA | AAGCTGTTTGGAARTTTCACAAAGAGTTTAAAATAGAATTACCTTTCAAGC |
| 572 | 1164 | CTGATTTCACTTATGCACATTTAAAGAA | P | TCCACAGTGCCATCCACC | | TTTCCCCACCAAAAGACAACTAATA | AAGTATTAAAGTACACCAAATTTTAGTATTAGTTGTCTTTTGGTGGGGAAA |
| 573 | 1165 | CGGGGATCTGGTTAAATGG | | CTCTGCTCCGGTCTCTGG | P | TGTCTCTGTTTGCTCCXTGAGATGCGA | TCTCTGTTTGCTCCATGAGATGCGAGCCCTGAGAGGCCAAAGCTATTTTTT |
| 574 | 1166 | TCACTGTCACGAGAATAGTATGGG | | CTCGAAYTGTAATCCGCATGT | P | GAAACTGCCCCCATGAGCCAATCAC | GAAACTGCCCCCATGAGCCAATCACCTCCCACCAGGTCCCTCCCTYGGCAC |
| 575 | 1167 | CAATCACYTCCCACCAGGT | | CTGATATGGTTTGGCTCTGTGTT | P | TCCCTCCCTYGGXACXTGCGGATTACA | CCTCCCTYGGCACATGCGGATTACAGTTCGAGGTGAGATTTGGGTGGGAAC |
| 576 | 1168 | TAATATCAAGAGGAGCTGCTGTCTTC | | CGTCCCAACAAATCACCACT | P | ATTCACTCTGAAAACTTACCTTTGT | ATTCACTCTGAAAACTTACCTTTGTGGACTCTTTGCCAAAGGTCTGTTCAG |
| 577 | 1169 | CTGGGAACGGTGAGGTGA | P | AGAGGCCATAGTTTTCAAGTAAGTCTT | | CTTCATTTTCTTTCATTTTCTGTGA | CTTATGTTTTGAATTCCCAAGGGCTATCACAGAAAATGAAAGAAAATGAAG |
| 578 | 1170 | GGTATCCAGCAGATATCATCATTATTA | | AGAAATCCTTTTTTCCTCAGCC | P | ATTGTAGATGTTGTTATTXTAGCCCAG | TGTAGATGTTGTTATTATAGCCCAGACAAGGGGATCTAGTGGGAAAGTGGC |
| 579 | 1172 | ATAGCAAGTCACCTTTACTCCAGTTTC | | GAAGATGTGGGAAGGTTCCAA | P | AGACCACCTCTGCCTTGACTTCATT | AGACCACCTCTGCCTTGACTTCATTGTCCATGTCACTATCAGCATTTTGGT |
| 580 | 1173 | ACCACTACGCCTGACTAATTTTTG | | CACTTGGGAGGCCAAGGC | P | TATTTTTAGTAGAGATGGGXTTTCACC | TTTTTAGTAGAGATGGGGTTTCACCGTGTTGGCCAGGCTGGTCTWGATCCT |
| 581 | 1174 | ACACAGACCCCCCAGAGG | | CTTGTCCAGACTCCCGGC | P | ACCTAAGGAGAACATXGGAGAGCCCAA | CTAAGGAGAACATGGGAGAGCCCAAAAGTCTCCTTGATTTGAGGAGACAGA |
| 582 | 1175 | TATGGTGACAGAGAGGTCAGCA | P | CAAGGCAATAATTGAGAATGCAA | | AACCTTTCAATTAAATAGGAGAAGC | GGTGGGGGCAAGAACTCTTGAGATGCGCTTCTCCTATTTAATTGAAAGGTT |
| 583 | 1176 | GCAATGACATTCCTCACAGAAATAG | P | ATTCAGGTAGTGTAATGTTTCCAGTTTT | | TTCCAGTTTTGTTCTTTTTGCTCAG | AAAGACCCCAAATAGCCAAAGCAACACTGAGCAAAAAGAACAAAACTGGAA |
| 584 | 1177 | CGGTACCANNGGGGATACTTTT | P | GCTGCCTAACGTGATGATAAGAGT | | CAAAGAAGCTGAAAGAAAAAGGTAG | AGACCCCNCTATGGACATCCCATTTCCTACCTTTTTCTTTCAGCTTCTTTG |
| 585 | 1178 | AGGCCATTCCCCCACCTG | | GTAGAAGGCTCACAGCTTTTGTG | P | TGTACAATGCCXGTCCCCCACCACAGC | TACAATGCCTGTCCCCCACCACAGCGGTAGTGCTGCAGTAGATTTTTGCTG |
| 586 | 1179 | CCAGGCAGAGACTTATTCTCATCTAG | | TGGCTACACTATACAACAGATGTTCAA | P | CTAGATAACATCTTCTTCCAATAGA | CTAGATAACATCTTCTTCCAATAGAGGGCTGTGTTGTCTACATTGAACATC |
| 587 | 1180 | AAACAAACATCCAGAGCCCTG | P | GTCTGCCTCCTCTGCTGC | | TGGGGTCTGCCTCCTCTGCTGCCTC | GCTGCTCCGGTCCCAAGGAGAGGCTAGAGGCAGCAGAGGAGGCAGAC |
| 588 | 1181 | AACTGTGAATAAATTGAGCCTCTTTATC | | TGGTACCTGTAAACAAGAACCATACC | P | AGACTCTXGTRAATACAATACTCTTGT | ACTCTTGTRAATACAATACTCTTGTGAACACAACCAATATATTTCTGGTAT |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 589 | 1182 | TTGAATTGTAGCTCCCATAATTTACAC | P | CTACCAAAAGAATAGCATGGGGA | | GGAAAACTGCCCCACAXTTCAATTC | GGTTGTGGGAGGGACCCGGTGGGAGGGAATTGAATTGTGGGGCAGTTTTCC |
| 590 | 1183 | GCGTTAATACTGATTCATTTATTAGCTCTAG | P | AGAGATGATAGTATCTTGCAGGTAGAAAAC | | TAGAAAACTCTAAACCCTAAACCCT | AGTTTTGTGYGTGAAGGGGGATCTGCAGGGTTTAGGGTTTAGAGTTTTCTA |
| 591 | 1184 | TGAGCCAAACTGCCTGAATG | | TCGAAAAGGAGGGGGCCT | P | TATTGCCTGTCAGTTTTGTTTCAAC | TATTGCCTGTCAGTTTTGTTTCAACGGCTCTTCATGTTTCAGTTCTTTTGC |
| 592 | 1185 | TTTTTTCTTTCTCTTTTTGTAGGTATGG | | GATCATTTCAGCCCAGGAGTC | P | TTTGCCGCXCAGGTGGGGTXCAGTAGC | TGCCGCCCAGGTGGGGTGCAGTAGCGTGATGATGGCTCACTGCAGCCTGGG |
| 593 | 1186 | AACAGTCTTTCCATATGTTTACCTCC | P | CATTTTGTCTTCTCACTGCACATC | | TCCXTCXTTCTCAGGAAGCCAGTCATT | ACCTGTCATGTAGTTGAAGTACCAGAAATGACTGGCTTCCTGAGAAGGAAG |
| 594 | 1187 | CTGTTTGTGTGTCTGCTTTTATGC | P | AGCCAATGCAATTCTGAGCA | | GAAXGAATATGTAGGCATCATACTACC | GATGTTTAATAGCTTGTAGTATATCGGGTAGTATGATGCCTACATATTCAT |
| 595 | 1188 | GCTCGGGGATAGTATGTGCA | P | ATTCAAATCTCTTGCCCATTTTTC | | TTCTATTGAGCTGCCTTTTTCTTAC | AGTCTACAAAAGATATTTATAGATAGGTAAGAAAAAGGCAGCTCAATAGAA |
| 596 | 1189 | ATCTCAGCTCACTGCAACCTC | | CATAATGAAACCCTGTCTCTACTAAAACTAC | P | GCCTCCCACGTTCAAGTGATTCTCC | GCCTCCCACGTTCAAGTGATTCTCCCGCCTCAGCCTCCCAAGTAGCTGGGA |
| 597 | 1190 | GAGCTGAAGAACCATCTCTGCTAG | P | ACCCAGGGGATCTAATCTTTTTT | | AATATTTAXAGATATTTGATAACTTTC | GTATGGCATGTCAGCATACGAAAGTCGAAAGTTATCAAATATCTTTAAATA |
| 598 | 1191 | AACATAGGGAGACCCCCCC | P | CAGAGATCCTCCTGYCTCAGC | | TAGCACTGCAGSCATXTGCCATCACAC | CCAAAAATAAAAAAAAAAAATAGCTAGGTGTGATGGCACATGSCTGCAGTCC |
| 599 | 1192 | TGAGGCACTTTGGTATTTCTCAG | P | GAATTACTCAGTCTCGGGTATTTCTTC | | CAGTGTGAGAATAGACTAATACAAG | CTCTTGTCCTGAGCACATAGTAGGTGCTTGTATTAGTCTATTCTCACACTG |
| 600 | 1193 | CCTGGCACCATTATACAAGCTACT | | CTGTTGCTGTTGAGGAGGGTT | P | TGCAAGCTXTGTGTGCAGAACCCAAGG | CAAGCTCTGTGTGCAGAACCCAAGGCGCTCTTCTGGAGTGAACTCCACAAC |
| 601 | 1194 | CACCAATTACCACAATTCTTGCA | | ACGATGCTATTGTTATTTCCCAAGTA | P | TTATTACCCTCGTTGTCTTCTCTCTCT | TTATTACCCTCGTTGTCTTCTCTCTGTATATCAATTCTTCAATTCTTCAAG |
| 602 | 1196 | CCAGACAAAATTATTACCTGTTTCCA | | TCACCAGGATTTTCAACTGAGAA | P | CTGTGTCTCCTGAGTGTGTCACCTC | CTGTGTCTCCTGAGTGTGTCACCTCGTTAGGTTCAATTATTCTTAAATTTC |
| 603 | 1197 | CACTTCACCTATAAAGACACATATAGACTTAAAG | P | ACCTAATATAAGTATAACAACTTCTGCTCACTCT | | CAACTTCTGCTCACTCTXGTTTCCATT | GAAGGGATGTGAAAAGACTCCACACAAATGGAAACCAGAGTGAGCAGAAGT |
| 604 | 1198 | TGTGGAGTGGTAGCAATGCTC | | GTGAGGGTGAAAAGGTAGCACA | P | AAGTXACCATTTGTAAGAGAGTAAGAA | GTTACCATTTGTAAGAGAGTAAGAACGGATTATTTGGTCCTGTCTTCTCTG |
| 605 | 1199 | GGCATAGAAACAGACACATCGAC | | TTCTTGGCACCTTTGTCAAAA | P | CCAGAGAGAAAGCCCAGAAATAAAT | CCAGAGAGAAAGCCCAGAAATAAATATAGTCATTTGTGGGCAATTGATTTT |
| 606 | 1200 | AATATCCTGTGTTCATGGATTGGA | P | ACTGTTAGGGCCTTTTGTAGTTCC | | TTGAATTTTGGTTAGGGATTGTATT | TACTACTTCAAGTGATCGACAGGTTGAATACAATCCCTAACCAAAATTCAA |
| 607 | 1201 | TGCAAACATTCCTTCTATGGCT | P | GAACATTCCCTTAAGCCAAAGC | | AAGCCTAATCCAGAGCAAGACCCTA | TCACCTCTCTCAGCCTTCAAGAGAGGTAGGGTCTTGCTCTGGATTAGGCTT |
| 608 | 1202 | CCTTACACTTTTATGTTATGAAAACAACTTG | | TGAAGGCTGAGAGAGGTGAGTAAG | P | CCTTAAATCTCATGAACCTACCTCT | CCTTAAATCTCATGAACCTACCTCTGCTAGTTGCAAACATTCCTTCTATGG |
| 609 | 1203 | ATTAGGTCACGTCACATGGCA | P | GAATCTTTCTTGAGCTCCTAATCCC | | CCGACCTCTACTCCCAGAXXTAAAGGA | AGCTTAGCCAATGGGCATGCCATAAGTCCTTTAAATCTGGGAGTAGAGGTC |
| 610 | 1204 | CCATTGAGTAAATAATGCGATTGTC | P | AGTCTCAGATATGTCTTTATAACAGTGTGG | | TAACAGTGTGGAGAATGGACTAATA | TATGTCATAGTGGCCCTTGAAGATTGTATTAGTCCATTCTCCACACTGTTA |
| 611 | 1205 | GCAACCTACGCAAGAGATAGGA | | TCCACACCTCTTCATGCTAGAAA | P | GGTAAAGAGAGAAACAAAACTATTT | GGTAAAGAGAGAAACAAAACTATTTATAACTCTTATCAATAACATTTTTCT |
| 612 | 1206 | TCTGTCTATGGAGCAGCCATTT | | CTGAAGAGAGGGAAGGCATG | P | TCTTTCACTCTTGGCTTGCTCTTGA | TCTTTCACTCTTGGCTTGCTCTTGAGTTGTTTCCTGAGTGAAGCCAAGAAC |
| 613 | 1207 | AAGCTGAGCCCCATGCCT | P | CTCCTTCCTTCTACAATCCCTTAA | | TGCTGAGTGGGCAATGAGGTAGGAG | TGAGATGGTGCAGCTATCTGCTTCACCTCCTACCTCATTCCCCACTCAGCA |
| 614 | 1208 | GTATACATAATAACATTCTCTATCACCCAA | P | TGTGTGTCGGGGTTGTTG | | GGTTGGGGTTGTTTGTTTTGTCAGG | GGTAAYGGAGGGAGTCACCTTTCCAACCTGACAAAACAAACAACCCCAACC |
| 615 | 1209 | GGCTAATTGTTCAGAGATTTATTTAACTAGC | | GGGTTGGGGTTGTTTGTTTT | P | ATAACATTCTCTATCAXCCAAAGGTAA | AACATTCTCTATCACCCAAAGGTAACGGAGGGAGTCACCTTTCCAMCCTGA |
| 616 | 1210 | TCCCTCCACTCCTCCAACC | | CTAACCCCTCTGTTCGATCTTTATAATAC | P | TCATGAGAAAGATAAGCACTCCCAC | TCATGAGAAAGATAAGCACTCCCACCACCAAGACCTGGAGGTGGGAAATGA |
| 617 | 1211 | TCCACTGTTGATGGGCACC | | TGCATGTTCATCGTGGCA | P | GGCTGACTCCATGTCTTTGCTATTG | GGCTGACTCCATGTCTTTGCTATTGGTCCATGTCTTTGCTATTGTGAATAG |
| 618 | 1212 | ATTGGTAGGAGGAGGACTGGAG | | GATCTGAGATGGATCTTTCTTTGC | P | CCTTGAATATCCGGAAATCTATGGC | CCTTGAATATCCGGAAATCTATGGCGTGGGATGCAGCTGGAGAGAACTGT |
| 619 | 1213 | GGTMAGGGTAGATGAGAAGKAGTCTC | | AGNCGCTTTGCTTTTTGTT | P | AGAAGAACAGAAATTCATAAAATAA | AGAAGAACAGAAATTCATAAAATAAGCTATAACAATCAGGTTAAACAACAA |
| 620 | 1214 | GGAATAAATATTATCTCATTTGATAGAGTGATTG | P | GAGTCCTCCCCAGCCATG | | WTTTTCTTTTGTAAGTTGTCCAGTC | TTAACACTGCTGATAAAGACATACCCGACTGGACAACTTACAAAAGAAAAW |
| 621 | 1215 | ATGGGTAGCAGAATCAGACTTCTTT | P | GTCCTGTTATCCTTTTCAGAGTCTTAGAT | | TAGATAAGGXGCTTTGCTCAGCCTGTG | GCACACTTTCCCGTTGCCTCAGCGCGCACAGGCTGAGCAAAGCTCCTTATC |
| 622 | 1216 | CAGGACTGGGTTTTATGTCTCC | P | ACCGGGGATCTTTTTAGTCTATG | | GATXTAATTAAAGATAGAATGGTTGTA | TTAACTATTAGATAATTAATATTCTGTACAACCATTCTATCTTTAATTAGA |
| 623 | 1217 | ACACCATCAGCATCAGCAAGA | P | CCCAAATATCTGTTGGATGAATAAAG | | AATTTAGAGGAGAAAGACATAGGTG | CCTCCTTGAGATCCTTTTGTTCCTCCCACCTATGTCTTTCTCCTCTAAATT |
| 624 | 1218 | ACTGTTGGGAAGGCATAATTGG | | CTCCCACAATATGTGATAATTCAGG | P | GTTTTGAXATGTGAGGACXTGAGATTT | TTTGAAATGTGAGGACATGAGATTTGGGAGGGGCCAGGGGCTGAATGATAT |
| 625 | 1219 | AGAACAGACTAATACAGTCAACTGGTACC | P | CCTCTGCCTGTTTCCCAGTT | | AGTTCCXAAGTCACTTCCXTGTTTTTG | GAGTGGGGCRTTGCTGAAAAGATACGCAAAAACATGGAAGTGACTTTGGAA |
| 626 | 1220 | GAGTTATTCAACATTACCATGAAATGC | P | TGGTTCCTACAAATGAAGACCAAT | | GCTTATCTGTTCGTGGTAGAAGTGT | TTTTTTAACAATCCTACCAATTTACCACACTTCTACCACGAACAGATAAGC |
| 627 | 1221 | GTTAAAGTGACATGTTCAGGGTCAC | P | GGTCCAGCGGAAGAAGGTT | | GAAGGGAXAAXCAGAAGTAAGATTCTA | TACCTAATTTGTTGCAAAGGTAGAACTAGAATCTTACTTCTGATTCTCCCT |
| 628 | 1222 | CAGGGGATGACATGGCAA | P | CTATTATAACAGAATACCACAAACTGGCTAA | | CTCACAGTTCTGGAGGCTGGGATGT | TTTGGTCCCTTGATCCTCAATCTTAGACATCCCAGCCTCCAGAACTGTGAG |
| 629 | 1223 | TCAAGCGATCCTCACACCTC | | CACTTGAACTCAGGAGTTTGAGAC | P | TAATTTTTGTATTTTTTATAGAAAC | TAATTTTTGTATTTTTTATAGAAACGAGGTTTCGCCATGTTGCCCAGTCTG |
| 630 | 1224 | GGCCTCAGTGAAGGTCTCCT | | CCACTCAAGCCCTTGTGC | P | TGCAAXGCTTCTGGATACACCWTCACC | CAAGGCTTCTGGATACACCWTCACGGCTACTGTATGCACTRCCAGGTCCAT |
| 631 | 1225 | AAATAAGGATTCCAGCAATCAA | P | GAAATTGGAGTATGATTGAGAAATGC | | GTGGTTGGGATTAAGGAAAGGAGGA | CCATAAACCCAGAATCTAATTATGAGTCCTCCTTTCCTTAATCCCAACCAC |
| 632 | 1226 | TATCATGAGGCAGAACTGTGAGAT | P | CAGGGTTTCACCTTCCCCT | | CCTTGGCTAGTTTGTCATTGAGATG | ATGATGGGTTCCTGGCTCAGCTTTGCCATCTCAATGACAAACTAGCCAAGG |
| 633 | 1227 | AAAACTCCACATGATGTTTGCAG | P | GTTTTCTTTCCTTGGAATGGTGA | | TCTGGAAAAGAAAGTAAGCACTGGT | CCTGGTAGTTTCAGACTCCAACTGGGACCAGTGCTTACTTTCTTTTCCAGA |
| 634 | 1228 | TATCTTCAGAAGGAGTTGGCTGG | | CCGGCAGCTCTGTGAACA | P | GTCTGTGAGAGCCAATGAACCCTTT | GTCTGTGAGAGCCAATGAACCCTTTGGAAGTTCTCAGATGGCCAATGAGGA |
| 635 | 1229 | ATCCTCCCAAACACCTTTGC | | AAATTTGCTTTGATATCCCAAAGTG | P | ATCAGTAGGCTCTTGTGAAGGAAAG | ATCAGTAGGCTCTTGTGAAGGAAAGATGGATGGCACTTCCCAGATATACCA |
| 636 | 1230 | GCTTTCCCAAGAGTTGGAATTG | | TGGTATCGAATAATGAATTGTATTCAG | P | ATTTGTATACTCATGCTGXACTACCTA | TTGTATACTCATGCTGTACTACCTAGTACAATGGCCTGTTGAGCTGAATAC |
| 637 | 1231 | AGGAAGCTGAAGCACGAGAAT | | TTTTCTTTTTTTTAAGACAGGGTCTC | P | CTTCAXCCAGAGAGGCAGAGGTTGTAG | TCAACCAGAGAGGCAGAGGTTGTAGCGAGCTGAGATCACACCACTGCACTC |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| | | | - | | - | | |
| 638 | 1232 | TTTAAAAAGTGGCTTTCACCTCAT | | CTTTGGCAGAGAAATGTTAGGAAG | P | TGTGAAGGCATGGGGAGAAATGTGA | TGTGAAGGCATGGGGAGAAATGTGAGTTATAAATAGCCAGGAGAAACTATG |
| 639 | 1233 | TTGGACAGCAAAGGGAAAA | P | GAGCTCTGAGAACTACAGACTTGACTT | | ACTTGACTTGCAAACACAGATTAGA | TAAAAAGATGTTCTTTGCCCTCCTGCTCTAATCTGTGTTTGCAAGTCAAGT |
| 640 | 1234 | AGGGCTACTGCTGCTCCAG | P | CCTGGCCCCATGACAGCT | | CCATGAACACCTGCACGACAGACAC | ACATGCCTGTTGGAGTGGTGGCTCCGGTGTCTGTCGTGCAGGTGTTCATGG |
| 641 | 1235 | AGTATTGAGAAGAAGGCTGGCAT | | CATCCTTTGAACTGGCAAGG | P | CTGGAATAGGAAXGTTTTTACTTACAA | GGAATAGGAAAGTTTTTACTTACAAAACAACAGCCAAGTCAGTCTGGCATC |
| 642 | 1236 | AGTATTCTTAGTAAGGGCTCGCA | | AGCTGGCAGGAAGCGGGC | P | GTCCCCGAATATGGCATTAGTACCC | GTCCCCGAATATGGCATTAGTACCCGATACCCGGCTGAGCTCAGACTTCCA |
| 643 | 1237 | CACCCCACCCACTTCCTT | | ACTGAATTTATTATAGCCTTCATATTTCCTG | P | GTGTGTAACAATTATTTGAAAGATT | GTGTGTAACAATTATTTGAAAGATTGAGTGTAACATTTCAGGAAATATGAA |
| 644 | 1238 | GCCATGTTTCACACTTTCTGTAATT | | ATATCCACCATGAGGACCACAG | P | GGAATGTTXATTTGTCTTGTATTAGTG | AATGTTAATTTGTCTTGTATTAGTGGAGGCTGCAATCAGTGATATTACTGT |
| 645 | 1239 | ACTGACACGTACCGCATTATAGTC | | CAATATGGAACCCGAACCAC | P | GCATGTTTACAAAACCCCCAGGCGA | GCATGTTTACAAAACCCCCAGGCGACACATGTGCACATTAAAGCTGAGACA |
| 646 | 1240 | AACATGGTGAAACCCCGTC | | CTCTGCCTCCTGAGTTCAAGC | P | AAAATACAAAAATTATCCAGGCGTG | AAAATACAAAAATTATCCAGGCGTGGTGTGGGTGCCCCGTAATCTCAGCTAC |
| 647 | 1241 | GAGCATCTGCCCCAAACC | P | TGTAGAACCATTTTGGTGTCTTGG | | CAATTXGTTCTTATACCAGXGCTATGT | AAATATCGCTTTCTAGAAGAGAAGACACATAGCTCTGGTATAAGAACCAAT |
| 648 | 1242 | CTCCCCATCCTCTAGTTCTCTATTTT | P | ACTACATTCTTATGCAAGTTGTAAAGGC | | TTGTAAAGGCTAAATCTCATAAAAT | CTTGGTGTTATGGCCTATATTAAAAGATTTTATGAGATTTAGCCTTTACAA |
| 649 | 1243 | TTTTGTGATAAGTTAGAATTAGGTAAGAGAACA | | CAATGGTCTTCATTCAGGTGCT | P | TTAAGCAAGATXCCAGGCAGAAGGAAC | AAGCAAGATTCCAGGCAGAAGGAACGTGGCAAGAGGGAGCAATAAAGGCCA |
| 650 | 1244 | CCTAACACCACCACTGAGAGC | P | CAAATACAATGATAGGAGCAAATGTCT | | GTAAAAAGCACTCTAAGAACCCAGA | TCACCAATTCCTCACCCGGCTCCGCATCTGGGTTCTTAGAGTGCTTTTTAC |
| 651 | 1246 | CCCGCTCCAACCTCAGAG | | CATTATTTTTTGTTTGCCAAGACC | P | GCAAATTCCCCGACATCAGAGAAGC | GCAAATTCCCCGACATCAGAGAAGCAGCCCTGGGCCACTAAACGGAAACCT |
| 652 | 1247 | CAAACTCCTTTTAATAAACTCTCTGCC | P | ACTCAGCAACTTTTTGTCTCCATC | | CTATTTACTCAAACAGGAAGAAAAC | ATACATTGAAAAAATAAATGCTCTCCGTTTTCTTCCTGTTTGAGTAAATAG |
| 653 | 1248 | GTACCTTACACTTGGCTGTATTCCC | P | GTGGAAGGCATTTACATCTTTGG | | TCAGTATCTTCCCXAACXTGGTTCCCA | ACTTTCTGAACCTGAACAGGAAACTGTGGGAACCATGTTGGGGAAGATACT |
| 654 | 1251 | CTGTTCTCTAGCCTGGGTGACA | P | TTCATAGTTGTTTCTGATAGCATTTCAG | | ACATATAAAXTTAAAAGATGAAATT | AATCTCTCAATTAAAAATGGATCCTGAATTTCATCTTTTAATTTTATATGT |
| 655 | 1252 | CTTATTTGTTCCCAATTCCGG | | GACATCTAATTAAATTGATCATCTACAGTGAT | P | AGTAAATTACAAGTATGAGCTAAGTTT | TAAATTACAAGTATGAGCTAAGTTTACTTTGCCAGTAGTGTTTGGCAAACA |
| 656 | 1253 | GGCTGAACTTAAACCATTTTACTCAG | P | AGGCAATCAGCACTCAAGAGG | | GTGGTTTGGTTTAAAACXAGGAAAAAA | TACAGTGCAACTCATAAGCAAATGAGTTTTTTCCTAGTTTTAAACCAAACC |
| 657 | 1254 | TGCCTAATGTACTACACATGATCGG | P | ACCTGGCACTCATGTCTCCC | | AAGGACTGTGACCTTTGTGAAAAAT | CGAAAAACTATTACAAATAAGTAACGATTTTTCACAAAGGTCACAGTCCTT |
| 658 | 1255 | TCCCAAATCATGACATTTTCTTG | P | ACATTTCTCTCAGATGTCCTTTTAGGTA | | CCTTTTAGGTATATACTXTGTTCACAT | ACATTTTAATGAAAACATGATTAAAAATGTGAACACAGTATATACCTAAAA |
| 659 | 1256 | TGGGCTGTACCCATTTTATTTG | | TCTCGCTTCTCATAGAGCACG | P | GGCAATCATTTAATTCXTGTTCATAGA | CAATCATTTAATTCATGTTCATAGAGGGAATATTTTAAGAACGTATAGGGA |
| 660 | 1257 | TGACGGAAACTTCCATAGAAGAAA | | GCCTGGGACCACTGCATAT | P | AGGGCTTTAAGAGCAGTGGTTGTTA | AGGGCTTTAAGAGCAGTGGTTGTTAAGTTTTCATTTATGTAGGAGACAAAA |
| 661 | 1258 | ACCACTTCTCTCTGTACTTTTTCTTCATT | | CATGCAGGATGAATATACAGAGTACCT | P | AAATGAGAGGCXGXGACCAGGCAACCCCGTGCATCTGGTGGCTGGTGACTCAG | |
| 662 | 1259 | TTGTCAGGGTATTTTCCGTAGAGA | | GTTTCTCGGCTAACACCCTC | P | CTCCAAATTACCTATGTGTGATCTA | CTCCAAATTACCTATGTGTGATCTAGTTATAAAGATTTGCAGGGAGCAGCT |
| 663 | 1260 | TTTAGTCCAAGGGAGTCCTGC | P | GAACAATGCAACGCCCTG | | CAAACATGAATCTGGGXACGGAAAGTA | TGACTACCGCCTTATTAGAGAGTCAGTACTTTCCGTACCCAGATTCATGTT |
| 664 | 1261 | AGAGATTTGATGTGGGACAGAC | | ACCAAGAAGCCAAAATATGAAATAAAC | P | ATTTTATCCCATTTCATTTTGACAC | ATTTTATCCCATTTCATTTTGACACCGGCTTTATTTCAGTTTTGGAGCAAA |
| 665 | 1262 | CTAACGAAATAATACCTTGATCACTTGAA | P | TGAAAGTTATATTTGGAATCAATGAGG | | AATGAGGTGATATGGTTTTATGCTT | CACATATACCTCATATACATACACACAAGCATAAAACCATATCACCTCATT |
| 666 | 1263 | AAGAAAAGTTTCCTATGGGAAGGAC | | CTGAGATTTGAGGCTACTGTAAATCC | P | ATGAGTATTAGTGGTCTTTCTGTCT | ATGAGTATTAGTGGTCTTTCTGTCTCCCTCAGGGCCACAAAATTCCCCTGG |
| 667 | 1264 | CATTCAAGATTTTTTCTGAAGTTATTTCC | P | TTTTAAAGGAACAGTTTGAAAACACTG | | ACTGTTGTTGTACAATCTGTGAAGG | ACCATAGTTGTGGGCTCTGAAATATCCCTTCACAGATTGTACAACAACAGT |
| 668 | 1265 | CTTGAGTCCTCCTCCATATCCA | | TTTGTTTTAGAACATTTCGCCTC | P | AATAACACATTTACATACACCGAAT | AATAACACATTTACATACACCGAATGTATCTTCTGTTAGAAAGGTGGAGGC |
| 669 | 1266 | ATCATCATTAGTCAAGCTATTCAGAGG | P | CATAAAAGCATTTGCTCCCTG | | GGTCACCAGGGAAACCAGGCGAGGA | CTCCCACCCATCTTCCAGGTCCCTCATCCTCGCCTGGTTTCCCTGGTGACC |
| 670 | 1267 | GGGGAGACTTCTATTTTATGGAAGAA | | AGCTATCTTATGGTAGAATAGCCACTTTAA | P | CATCCTCAGTGATTGGAAGATTATC | CATCCTCAGTGATTGGAAGATTATCACAATGGAAAGGCCTTTTAAAGTGGC |
| 671 | 1268 | TTGCATTTTCTGATCCTTCATCC | | GAGAGAGGGGTGCCATTTACA | P | AATGTTCTTCCCTCAGTCACCCAGA | AATGTTCTTCCCTCAGTCACCCAGAGGATGTTTTCCTGAACATCATTCAGG |
| 672 | 1269 | ATGAAGTCTTATGAGAATTGCCTCTTATT | P | CAATCCCCCATTCATCTCAG | | GTCAGGGTGAGTTGAGTTTGGGTAG | CCCCAGTGCTGAGATACACAAACTTGCTACCCAAACTCAACTCACCCTGAC |
| 673 | 1270 | CCAAAAAGCAATTAGGCATATAAATAAC | P | AGTGAGTCACCTGTAGACAGCGTAT | | TTGTTTAXATCCATTCTGCCAATTTGT | TGTATTACACTCTTCAAATGAAAGACACAAATTGGCAGAATGGATTTAAAC |
| 674 | 1271 | TCTGAAGTCGAAGTACTCGCC | | CTAAAGTCCAGCTTCTCATGCTG | P | GAGGTCCGTGCGCTGTGGTAGCAGG | GAGGTCCGTGCGCTGTGGTAGCAGGGGGGAGCCCCGCCAGCCAAATGCCAG |
| 675 | 1272 | GTTTAGCAAACTTTGACAGGCAA | P | TGAGCAACTCAAAAAGAGAAAAACA | | AAAAAAAAAAAGAAAAAAACCCTGA | GTGAACTGATCTTATAGGAGAGATTGTCAGGGTTTTTTTCTTTTTTTTTTT |
| 676 | 1273 | ATGCAGAAATCCTCAGCAAAATATTA | P | CCTTGCATCCCAGGAACA | | CAAAGCCXACTTAATTGTGTTGGATTA | TCAAATCCAGCAGCACGTCAAAAAGCTAATCCAACACAATTAAGTGGGCTT |
| 677 | 1274 | CCAGTGATTCCACAGTACAAAAGAG | | ACAGAAATGCAATATTCGTTACAAATG | P | TCTTCTTGTAATATAACATTTCTGA | TCTTCTTGTAATATAACATTTCTGACTTTAAAGAGATAAAGTATCAACATT |
| 678 | 1275 | GAATTAGTCTCTGAGGGCATGAACTA | P | TGCATAACTATTGTATGCCAGGC | | GGCACTGGATCAAGGAATACAAAGT | TTTTATTCATCTTTATATCTTTATACACTTTGTATTCCTTGATCCAGTGCC |
| 679 | 1276 | CAGGAGGTCAATGCCGGG | P | CAAACTTCTCCATCGCCCTT | | AGAGATCCAACCACTCAATCCTAAG | CTGCATCCCACCTTGCTGATGAGGAGCTTAGGATTGAGTGGTTGGATCTCT |
| 680 | 1277 | ACATAGGGTATCTTATGTCCCAGGA | | TTGACACAAAAACATCTGAACTAAGAAC | P | CTTTGGAATGXACAGGTACAGGATCTC | TTGGAATGTACAGGTACAGGATCTCGGAATCTTAAGTTTTGGTTGTTCTTA |
| 681 | 1278 | TCTTTTACTGTGTGCACTGGTGA | | CTCAAAAAACAAGACAAAAATGCAC | P | ACTGGCTGCTAGGAGAAAGTGTGGT | ACTGGCTGCTAGGAGAAAGTGTGGTCCCATAAGCAAATATGTGCTTTACAT |
| 682 | 1279 | GAGAAGTTTTCTAATATCCTTTAAGTTGCTATC | | TTCATTTCCTCTCCAGAACCC | P | ATTCTGATAAATGGATTGAACTATG | ATTCTGATAAATGGATTGAACTATGCTTCTATAATAAAATAATTATATGGG |
| 683 | 1280 | AGTTTGGGAAGAACAAAAGCTCA | P | AATTCAAGTTGAGATTTGGGTGG | | GGGTXGGGACACAGCCAAACCATATCA | TGAATTGTTGTTTTGCACTTACTCCGTGATATGGTTTGGCTGTGTCCCCAC |
| 684 | 1281 | ACCCTGAAAATCACCCAAATC | | CCTGCCAAGACATACACCATC | P | ATAGTTTCAAXTAGAGCAATAGTAATA | AGTTTCAATTAGAGCAATAGTAATACTGATCATGTATCAAAGAAAAATGCC |
| 685 | 1282 | ACACCTGAGTAGACCTCAGAGCC | | GTTCAGTGAACATTAGAGGGCAG | P | AACXACXAGATGCATTTGGCAGTGTAG | CCACCAGATGCATTTGGCAGTGTAGGGGCCAAGGGAAAGCATTCTTTCTGC |
| 686 | 1283 | ACTCCAAGTATTCCTTTGCAGATTC | | CAAAGTGAAATATCCTCACAAAAAAAGTA | P | GAGCGGAATGCACACATCACAAACA | GAGCGGAATGCACACATCACAAACAGGTTTCTCAGAATGCTTGTCTACTTT |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 687 | 1284 | CACAATCAGGTCTGATTTTACCAAA | P | TGCATTACACTAGTATGAGAGAAATACAGAA | | AGAATGTCTGTTTTGXAXTTCCATG | AACTTAGAAATACTTCTAACTTAGGGCATGGAATTTCAAAACAGACATTCT |
| 688 | 1285 | TATGTGACTTGCCTGTATCTCACAG | P | CATTTCTCTGTAAATTTCACTCTCCTC | | AATGCTCAGCCXTTTAGGAXTAGATAT | CAAACCTGAGGTTCTTAACTACTATCATATCTAGTCCTAAAGGGCTGAGCA |
| 689 | 1286 | TGTATATGGTGAGAGAAGGAGTCTAGTCT | P | ATGCATTGGAAAATAAGGTAGTCTCTT | | TAGTCTCTTAAAAAAAAAAAAAAAG | CATGCAAATATTAAATTTTCCCAGTACTTTTTTTTTTTTTTTAAGAGACTA |
| 690 | 1287 | CACTTCCTGTGACACCCCC | P | GTCATGAAGGTGGGTGGG | | GGTGTGAGCCCCCTTGCTGGAGAGT | AAACCTCGGCCCTCCTATCTTAATACACTCTCCAGCAAGGGGGCTCACACC |
| 691 | 1288 | ATGAATGAATGAGCAGTAGGCAG | | CAGAATACCCCAGAGACTCAGACC | P | GCCTGTGACXAGGTGGTTGGGGACGAG | CTGTGACCAGGTGGTTGGGGACGAGCCCCCCTCAGATCAGCCCCAGGTCTG |
| 692 | 1290 | CCGCTCCTATTGCTCTCTAAAAA | P | GGGATGATTTAAAAGAGATAGATAAGTATATGC | | AGTATATGCAGCAGTGTATAGACGC | TTTCTATGGGCATGCAATATTAGATGGCGTCTATACACTGCTGCATATACT |
| 693 | 1291 | AATGGAGCCCACTATCACAAA | P | CATCAGAAACCCAGAAACCTG | | CTCTCXCXCGTGAGAGGTCTGTGTGGG | AAGGTCAGGAGGGCCTTTCCCTGGGGCCCACACAGACCTCTCACGGGGGAG |
| 694 | 1292 | AAATCTCATTTTGAATTATAGCTCCCA | P | CATCGAGATCTTGTGAGATGTATTCA | | CTCATGATTCAGTTACCTCTCACCA | AATCCCCATATGTCATGGGATAAAGCTGGTGAGAGGTAACTGAATCATGAG |
| 695 | 1293 | AAATCTCAGGTTCCCTCCCA | P | CTAAATGCGGAAGACAGCAGAG | | AGAGAGCAAGGCTGGGCGGCACACG | CTGAGTCCTGCACATCTCACTCCAGGCGTGTGCCGCCCAGCCTTGCTCTCT |
| 696 | 1294 | AGCTTATCCAATGACTATCTCTGAAAATAA | | GGGGCATATGTTATGAGGATTCT | P | CACTAACCCTCTTATCTAXATGTGCCC | CTAACCCTCTTATCTATATGTGCCCGGCACTTGCCACACAGACATGGCGAG |
| 697 | 1295 | ACAAGAATTATTCTGTCACATGATATGG | | TAATAATAATGTGTAATGTTTATCCTGACTCATC | P | GAGAGCACGAAAGAACCACATGCCC | GAGAGCACGAAAGAACCACATGCCCGGGCCCTCAGCATTAGATGAGTCAGG |
| 698 | 1296 | AATCAAAAAGAAAGGAGGAGAAAGAA | | CTTAAAATTTCTATGCCCTCTTGTCTC | P | TCAGGAGAAGTTTTTCAGGGTGTTA | TCAGGAGAAGTTTTTCAGGGTGTTAGAGGAAAGGGTGGGAGAACCATAGGG |
| 699 | 1297 | ACTTTGTTTTCTGCCAACTGCA | P | GAAGCTGATGATTGAAAAACTCCTC | | AACACGTGAACCCACCTGACTTACT | GAAGACAAAACAGATGAGGAACACACAGTAAGTCAGGTGGGTTCACGTGTT |
| 700 | 1298 | TATCATATATAATATCAACCGAAACAGACAG | P | GATAGAGGTCCCTGACTCCAGAC | | ACCACAGTTAATGGGGGAGATAGAC | AGCCAGCAGTCTAATTGCTCATATGCGTCTATCTCCCCCATTAACTGTGGT |
| 701 | 1299 | GGGAGAGAGGGAGGAAGACT | | AGCGTCTGTTTAAATAGCCTCGA | P | GCCAGGAAGAACAGAGGGAGGAAGA | GCCAGGAAGAACAGAGGGAGGAAGACCTGCCAGCAAGAACAGGGAGTCGAG |
| 702 | 1300 | TATCTACTCAGAAACCACGCACAA | P | CTTGCAGGGACAGTGGCTT | | CTCTCGAGTCCATGTCCCGCCGCAG | GGAGCACTGGGTCTTTGGAGTCCGGGCTGCGGCGGGACATGGACTCGAGAG |
| 703 | 1301 | TGTTCCAAGACATAAAGATCAGGAG | P | GATGACAGAGGTGGTCATGGC | | TTCTAGATGGCTGTCAGGTGGTGGG | AGAAAAATTCAATGTAACTAAAGCTGCCCACCACCTGACAGCCATCTAGAA |
| 704 | 1302 | TTGGTGTAGAAGAGAAGCAAGAGAG | | CATATCTCTACAGAAAACCCACATTG | P | TTGGGTGGCCCAGGCACTAXCTGTCCT | GGGTGGCCCAGGCACTAGCTGTCCTGTCAAGGGGCAGAGCTCTCTGCAATG |
| 705 | 1303 | AAGATCATTCTTCCACGCCTAAC | | GAATACGGTGGTCTCTGGAGTC | P | AATTGCAGTAACTCGCCTTTGGGAG | AATTGCAGTAACTCGCCTTTGGGAGGGAGAAAGGAAAAGGTAGGCAATTTA |
| 706 | 1304 | AGATGACCCCTGATGGTTAGCT | P | CAAGGAATTTCCAATGCTGTTG | | AAAAAATAGTTAATCTGTTCAGTTC | AGCCCTCATTGAGTGCATCCTGACACGAACTGAACAGATTAACTATTTTTT |
| 707 | 1305 | GCTTTTGTTGTTTATTGTTTAAGACATCA | P | AGGTGAATCGATCTGTGTGGTG | | AAAATCAGTAACAAAAATAACATCA | TTCATTGAAGCTGTCTCACAGCTACCTGATGTTATTTTTGTTACTGATTTT |
| 708 | 1306 | TGTAGCTGGGACTACAGGCAT | | GTAATTCCAGCACTTTAGGAGTCC | P | GATGCCCAGCTAATTTCTCTTTTTT | GATGCCCAGCTAATTTCTCTTTTTTAAAAAAAAAATTGAGATCGGGTCTTG |
| 709 | 1307 | TGGCCTAGCCTCTTCCTCTG | P | AATTTAACAGCGTGAAAGAACAGATT | | AGAAXAGXTTCGATGCAGGCTATCTGT | CCCTTCTTCCAGGAGCCAGCATGCCGACAGATAGCCTGCATCGAATCTGTT |
| 710 | 1308 | AGGTGGCTCTATCTCAGAGAGGA | P | TCTGCTTGACTCTGAAAATCACATT | | ATCACATTCTTXGCTACTATGCTATAA | GACTATAAAGGGTAGATAAATATTACTTATAGCATAGTAGCTAAGAATGTG |
| 711 | 1309 | GGGGTGACAGTATGTATGTAACCAT | | ACGGTTTAGTTTCAATCTTAGAACAGTT | P | CTATGCCCATTCACAGATXCAGTAGAG | ATGCCCATTCACAGATGCAGTAGAGAGAAGAATTTCTTAAAGACAACTGTT |
| 712 | 1310 | TCCTTCCCCAAGAGCAGC | P | CAAGGTCACAAAGTGAGGAGC | | AGCXAGCAGCGGAXACTTGTCTATGTG | GAATTCCCGAGGCTATGCTGGGATTCCACATAGACAAGTCTCCGCTGCTTG |
| 713 | 1311 | GCACAGCCAAGTCTGAAAGTTT | | TGTAGTTCTGAAGTGTGGGACTTTAAA | P | CAACAAATTGGTXCAAAGATGAAATAT | ACAAATTGGTTCAAAGATGAAATATGTATCAATATATCTAAGAACCCTTTA |
| 714 | 1312 | AAATCTCCAGACCAAGAAGAAGC | | AGAAAGAAAGAAAGAAAAAGAAATTGAGG | P | TATAGACCTGATGGAGAGCACTACG | TATAGACCTGATGGAGAGCACTACGCGGTTCACTTGAAGACCCTCAATTTC |
| 715 | 1313 | GTCAGACAATATGCAGCAGTGTAAC | | AGGAATGAGTGTACCATTCTTTATTCAC | P | TGTAATTAATATCTCAAAAAGGATG | TGTAATTAATATCTCAAAAAGGATGGGTGGGGGAATTATAGGTGAATAAAG |
| 716 | 1314 | GCACAATCTCCCCTCATTG | P | GGCACCTGTAATCCCACCTAC | | TACTCGGGAGGCAGAGGCAGGAGAA | AACCTTTGCCTCCAGAGTTCAAGTAGTTCTCCTGCCTCTGCCTCCCGAGTA |
| 717 | 1315 | AAATTACTCAACATCACTGACTTTTAAGATAC | P | CATGTTAGCCAGGATGGTCTC | | GATCTCCTGACCTCGTGXTCCACCCAC | TAATCCCACCCCTTTGGGAGGCCGGGGTGGGTGGATCACGAGGTCAGGAGA |
| 718 | 1316 | TGAGCAGGGGGGATGGGT | P | AGGGACAGCACTGGACTTCC | | TTCCATCTGXAGAGCCCCCTCCCCTCA | CCCACCTAGCAAGCAGGTGCTGAGAGTGAGGGGAGGGGGCTCTCCAGATGG |
| 719 | 1317 | TCCAGGGTCTGGGTCTGC | P | CATCGCTAACCAGGCCCA | | CTTXTGCTCACCCAGCCACXCTCAGAG | TTTCTGCTTTGGCCCACCCTCCAGGGTCTGGGTCTGCAGCTCTGA |
| 720 | 1318 | TTGAGGCCAGGAGTTTGTGA | | CAAGTAGCTAGGACTACAGATGTGTGC | P | TAGCGXGACCCTTATCTCTACAAAAAA | GCGAGACCCTTATCTCTACAAAAAACTTAAAAATTAGCCGGGCATGGTTGC |
| 721 | 1319 | TTGAGAGGGCAAAGCATAAT | P | CATGATTCAAGGGGGAAAGG | | AGGAACCTGCAGCAGTCTXTAATAAAC | AGTTTGTGGCCAGAGGACAAGCTGTGGTTTATTAAAGACTGCTGCAGGTTC |
| 722 | 1320 | TTTTGTGACCAGGTTAAACAAAAAGTA | P | ATTACAGGCGTGAGCCACAA | | CACCTGGCCTCCATTGTTCATTTAT | ACCAAAAGCGTGATTCCTAAAAGTCGATAAATGAACAATGGAGGCCAGGTG |
| 723 | 1321 | CTGCGCCTTCCTCTGCTC | | CCTCCACCTGCTGAATACTAGTAGC | P | CTTCAACCATTTCACTTCTTTCGTG | CTTCAACCATTTCACTTCTTTCGTGGCCACCACTTGGCTGGGATGCTACTA |
| 724 | 1322 | TGTTATTCAGATAAAAGACTGAGTTATGCA | P | CAAGGAGTTTATGATCCCATAACTGA | | GAATGAATGAATTTGCCGATGTCAG | GTGGGGGAGAGTGCAAGCATGAAAGACTGACATCGGCAAATTCATTCATTC |
| 725 | 1323 | ATGGACAGCTATGACATGATTACG | P | GTAGTCCCACCTATTCAAGAGATCAA | | GTACAATTTCAGGTTCTCTCTATCG | CCTGCAGGCATGCAAGCTTGTTATTACGATAGAGAGAACCTGAAATTGTAC |
| 726 | 1324 | TTCAACATCCTCCAGGACAGC | | CATATCGAGCCCCTGTCCC | P | ACAGTATCTGGTCCAAATGTCAACA | ACAGTATCTGGTCCAAATGTCAACAGCGCCAAGAGGGACACACCCTGCCCT |
| 727 | 1325 | AATCTTCCTGCCTCAGCCTC | P | GAAGGTCAAGATTGGAGGTTTG | | AGTGAGACTCTGTCCCTAAAAAAAA | CACTACACCTGGCTAAGTTAAAAAAATTTTTTTTAGGGACAGAGTCTCACT |
| 728 | 1326 | AGATTTTGTTCTACCTATTCCTAAGATCTGT | | CTGTGAGGATTAAATAAGTGAATGCA | P | ATTTTTTTTCCTGCGTGCCAGATAC | ATTTTTTTTCCTGCGTGCCAGATACGGAAATAAAGACTTTCTGTGCATTCA |
| 729 | 1327 | TATAAAAGGCTTATTTCAGTTAGAGAGTGTTC | P | CAGTCTCGGGGGCTGATC | | GGTAAGGGAATGATCTACAGGGTCT | CGACCAGAATCCCATGACCAAGGGACAGACCCTGTAGATCATTCCCTTACC |
| 730 | 1328 | AACTCCCCTCCTGCTCAAAC | P | CTGGGCTCCCATCTTCAAG | | AGAAGATCCTTAACAXTXATTCTGT | CCTGCAGGCATGCAAGCTTGGTGGAAACAGAATTATTGTTAAGGATCTTCT |
| 731 | 1331 | ATGCTACTAATTCTTGGTCAAAACCC | P | CTTTTATAAGTTATGGCTGAAGACAAAGG | | TGTAATCCTAAATAAAACTXCGGTCTC | GTCGACCTGCAGGCATGCAAGCTTTAGAGACCGGAGTTTTATTTAGGATTA |
| 732 | 1332 | ATCATCGCAGGGGTGGGG | P | CCTTACCTCTCTCACAATAGAATATCGTAC | | AGAATATCGTACGXCGTGXGCTGGCAA | TAGAGTCGACCTGCAGGCTTGCAAGGTTGCCAGCGCACGGCGTACGATATT |
| 733 | 1333 | ATGACAGTTTGACATGATTACGAATTC | P | CTCCACAATGCTGGTTCCTAG | | GGCAGGATTTGAACCCTAACTCTGA | AGAGTCGACCTGCAGGCATGCAAGCCTCAGAGTTAGGGTTCAAATCCTGCC |
| 734 | 1334 | CCTAAGCCACCTTTGGCAT | | ATAAGCCGTCTCCTCCATTTACC | P | TATACATTCTATTCTTAGTCATTTT | TATACATTCTATTCTTAGTCATTTTCTCCTTGTTCACCTGAGTTTCCTTCT |
| 735 | 1335 | TGATGGGAGCTCTGTGTGG | | CTTCCGTCATGAACTTTGGC | P | GGCXCXCAGTGAGCTTGATAAGGGAGG | CCCCCAGTGAGCTTGATAAGGGAGGAGAGGCTGAGAGCTGGTTCCAGCCCG |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 736 | 1337 | TTCTTGCTGGGGAACCTCA | P | GAAAGAAAGAAAGAAAATGAATTTTGG | | TTTGGCATAAAAACTTGGGTCTCAT | TGTAAAAAGCATATTGGTGGGAAAGAATGAGACCCAAGTTTTTATGCCAAA |
| 737 | 1338 | TGAGGTCGGTGCTGGACG | | CGCCACCACCCCAGGAAC | P | CGAGTACACGCGXCCAGTACACAGGGC | AGTACACGCGCCCAGTACACAGGGCGTGAGCTCATTACACGCCCCAGTTCT |
| 738 | 1339 | TGTAAAATGATTATGATTACCACACTCAA | P | GATCTCAAGTGTCCTACACATGCA | | ACACACACACACACACACACACGGT | TAACACATTAATTACCTTACCTAGTGACCGTGTGTGTGTGTGTGTGTGT |
| 739 | 1340 | TGTAAAATGATTATGATTACCACACTCAA | P | GATCTCAAGTGTCCTACACATGCA | | CACACACACACACACACACACGG | AACACATTAATTACCTTACCTAGTTACCGTGTGTGTGTGTGTGTGTG |
| 740 | 1341 | TGTAAAATGATTATGATTACCACACTCAA | P | GATCTCAAGTGTCCTACACATGCA | | ACACACACACACACACACACACG | ACACATTAATTACCTTACCTAGTTAGCGTGTGTGTGTGTGTGTGTGT |
| 741 | 1342 | CATGCCCAGCCTCAACAT | P | AGATGGAAGTAATGAAATTTGTGTATGTC | | ATTTGTGTATGTCAGTGATXACGGTAA | AATGCGAGACTTAAATCTACTCATGGTTACCGTAATCACTGACATACACAA |
| 742 | 1343 | ATCCACGCCCTACAAAGGG | | CATAGAGAAGGCAGAACCGAGA | P | CTTTCCTGTTTCATAAGTAGCAATC | CTTTCCTGTTTCATAAGTAGCAATCCCTGTGGTAACAGCCCCTGTGGTGAT |
| 743 | 1344 | AACTCCTCTATCACACACCGATGT | P | CAAAATATGGAAAAAGCTCTCAATTG | | GCATTGTCGACTGGTGTTGATTTAC | TTTCGGCATGACACAAAGCATGAGCAGTAAATCAACACCAGTCGACAATGC |
| 744 | 1345 | ATGTAAAATGAATGGCAAGGCA | P | CATTGCTGTACCTGGAAAATGG | | GGGCCCACAGTAGCATTCTXCACTACA | TCTTCATCCCGACGGCAACATACGTGTGTAGTGCAGAATGCTACTGTGGGC |
| 745 | 1346 | TCATGGCAAAAGGCAAAGG | | TTGTTTAAAAGTGTGTAGCACCTTCC | P | GGGAGTGAGGAGGXGTGAACACGGCAG | GAGTGAGGAGGTGTGAACACGGCAGGAACAGGAGCAAGGTGCAGGAAGGTG |
| 746 | 1347 | CTTAAATGAGTATAGCTGATGAATCAATGA | | CCAAAATTGTCACAAGTCTTTGATT | P | GACAACTTTGGGCAGTGGGTCTCAA | GACAACTTTGGGCAGTGGGTCTCAAAGAATTCAGCTTCCTAGGCCTTCAGA |
| 747 | 1348 | TTCTGTGCCTATTGGGGTGA | P | CAAACTGTCTTTTTCTCATTCCTTTG | | TTCCTTTGTCTCCTCTGGACTTCGT | CAACCAACACCAGGTCGTGGGGCGGCGACGAAGTCCAGAGGAGACAAAGGAA |
| 748 | 1349 | GTTTTTCAATATAGTTTGTTACCTATTCACAC | | TTTCAAGATGACAACAGAGACATTAAATAT | P | CAATTATTTTTCCTTTTTCAAGTGA | CAATTATTTTTCCTTTTTCAAGTGACACATTCAGCATAACCTGAAAGATTA |
| 749 | 1350 | TATCCATGATACTTGTTTGTGCTCTC | | GTACACCAGAGAAACAAATGCATG | P | AGTAGGTCTCCTGTCATCTCAGCAC | AGTAGGTCTCCTGTCATCTCAGCACGAGGTACCAGTGCCTTTGGTTCATGC |
| 750 | 1351 | ATATTTTCCAGGGAGTAATCTTTATATTTGG | | CATCTAAATCTGGAGCTACCCAGA | P | TTACTCTCAAGGGATAGTXCAGCATGT | ACTCTCAAGGGATAGTGCAGCATGTGCTTTTAAAATGCCCTTCAGGACTTG |
| 751 | 1353 | TTTTGAGATGGATTTTTCCTCTTG | P | CAGGAGAATCACTTGAACCTGC | | ACCTGCGAGATGGCGGTTGXTGTGAGC | GGCTGGAGTGCAATGGCAAAATCTCGGCTCACAGCAACCGCCATCTGCAG |
| 752 | 1354 | TGTTTGTTCCCCCTCTGGTAG | P | CTATTTCCATCTTCCTATCCCCAG | | GCTACGTGGTAGCCTXGAAAATCAACA | TTTTATGACTACAGTAATTGCAGGGATGTTGATTTTCAAGGCTACCACGTA |
| 753 | 1355 | GGGATAGGAAGATGGAAATAGAGC | P | GATTCCTCCATGAAAACAATCAGA | | TTATCACAACTCTGAAGGCTAACCA | AACACTTCTCAGTTTATTGAAAGCCCTGGTTAGCCTTCAGAGTTGTGATAA |
| 754 | 1356 | CCCTCTACCAATTTCTATATAAGTCAGGA | | TGAGTATAATACCAGAAGTATGACTGTTGATC | P | TCATAACAAAAACCCAAATCTCAGA | TCATAACAAAAACCCAAATCTCAGAGAAAAATACAACAAAAACTTATTTTA |
| 755 | 1357 | CCAAAGTCGAGTATGTTGCCA | | TCCAATCTGGTTGGTAAATAGCC | P | ACAAATAAAAAATGAGGCAXATAGGCA | AAATAAAAAATGAGGCATATAGGCAGCTCTAGACAAGGTCTGGAATGGCTA |
| 756 | 1360 | CATCTTAAGTGGTACATTTAAGTATTAGCTCC | | AGCTAAGTAAGTGACACATCAAAAATATCA | P | CTCAATGAAATATGTAATGTTTTAT | CTCAATGAAATATGTAATGTTTTATAATTGTTCAATTTTTAAAAAAATTTC |
| 757 | 1362 | AACATCTTACAGCAGATACTCCTTACACA | P | AGCAGGGAAACTTCCTGTCAG | | CCTCCTACAXTTAGAATTGGGGGAATT | AGGCAATCCTCTTGTTATTTTCGAGAAATTCCCCCAATTCTAATTGTAGGA |
| 758 | 1363 | GTCTTTCTGCTTCAGCCTTCAG | | GATATTAACAATATCTTTAATGRCATGCCT | P | ATTXCATATCTAATCAGTGTAACAACA | TACATATCTAATCAGTGTAACAACAACAGCTACTTAAAGAAGGCATGYCAT |
| 759 | 1364 | TGAGCGGTGGGGCTGGAG | | GTTTCACCCATTCCAAAAGTCC | P | TCAGAACAAGGGATGGAGGTCTCAG | TCAGAACAAGGGATGGAGGTCTCAGAGTTATCTGGCTGGATATGAGAGTTG |
| 760 | 1365 | GCCCTGAAGACTAACACACAGC | | TGAGGTCTCARATCTGCCATC | P | AAGTTAACCTCAATGCTCXTGTGAGAT | GTTAACCTCAATGCTCATGTGAGATCAGTGCTATTTCCACTTTAAAAGGAA |
| 761 | 1367 | CAACACAGCATCAGCAGTTCA | P | TCGAAGTTCCCTTTGCTTGTC | | CAATAATGTGCATTGTGTTGAGTTT | AACAAAGGTAATATGTCTTAATATAAAAACTCAACACAATGCACATTATTG |
| 762 | 1368 | GATGTACTGCTGAATACAGTTCGC | | TGTCACTCAAAATTCCCAGGA | P | AGTATTTGGTTGAGGATTTTTTTAT | AGTATTTGGTTGAGGATTTTTTTATCTGTCTTCATCAGAGATATTGACCTG |
| 763 | 1369 | GCTATGACCCATGCCCCG | | TTTACCAATGTATATGTTTATGTGTGTTATGC | P | CACACATAGATATATXCACAAGTATAT | CACATAGATATATGCACAAGTATATGTATATATGTGTGCATAACACACATA |
| 764 | 1370 | AGAGGGGAATATACTGTCTCTCAGTAAGT | P | TAGAATTGATTTTTGTGTACGATGTAATGTA | | GAGTCGTTTCTTTTTTTMCCCCCCT | ATACTGGGACATCTGGATATGCATACAGGGGGGKAAAAAAAGAAACGACTC |
| 765 | 1371 | AGAGGGGAATATACTGTCTCTCAGTAAGT | P | TAGAATTGATTTTTGTGTACGATGTAATGTA | | TAATGTAGGAGTCGTTTCTTTTTTT | ACATCTGGATATGCATAYAGGGGGGGAAAAAAAGAAACGACTCCTACATTA |
| 766 | 1372 | TGCCAGTCCTAAAATTCCCA | | GTGACCAGGGTTGTTGGC | P | AATTAGTTCATTTTTAXAGTTTCTATA | TTAGTTCATTTTTATAGTTTCTATAGAAATAATTTTTTCCTATAAAAAACAA |
| 767 | 1373 | CATGCCACTGTACTCCAGCC | P | ACAGGACATACAGAATTACTTTCAAATGA | | AGTATGTATGTAGGTATGTATGTAT | CAAGACTCTGTCTCATAAATACATAAATACATACATACCTACATACATACT |
| 768 | 1374 | GAAAAAGATGGCAAGTACACACAAT | P | GGTCTAATTTCATTTTCTCTGCATGT | | CATGTGAATXTTCATTTTCCTAACACT | GTGAATGGACAGCCTCTTCAATAAACAGTGTTAGGAAAATGAACATTCACA |
| 769 | 1376 | CTCTTGGCATCATTATGGGC | | AACCTCTAAAACATGCTACAGGTAAACTATTA | P | AAAAGAATGGAAAATCAATCAGAGG | AAAAGAATGGAAAATCAATCAGAGGGCCTGGGCATTATAATAGTTTACCTG |
| 770 | 1377 | ACATGTCTCTATCTCAGCGTTCCT | | CTTTAGGAAGGTCACAATTCAGGC | P | TCCCAACACTCATCAAGCCCATTAT | TCCCAACACTCATCAAGCCCATTATATTTTCCCATGTGGCCACAATCTGTT |
| 771 | 1378 | AACTTTTCTGTCTAGCTAAAGGATTGTAAAC | | GATTGGTCCATTTACAAACCCTTAG | P | TTGTAAACACACCAATCAGCACTCT | TTGTAAACACACCAATCAGCACTCTGTAAAAACGCACCAATCAGTGCTCTG |
| 772 | 1379 | CTCAGTGGAATTGTGTCAACAGG | P | AATTTTTTTTGGAAAAAAGGTCTCTG | | GGTCTCTGCTTTTTCTATTTTGGAT | GACTGAAAAAAATTMTCAGAAACAGGATCCAAAATAGAAAAAGCAGAGACC |
| 773 | 1380 | CTCACACCTGTAATCTTGGCA | P | CTTGATATGTTGCCCAGGCT | | CTGGTCTCAAACTCCTGGGCTCAAG | TTGGGGCGGCTGAGGCAGGAGGATTGCTTGAGCCCAGGAGTTTGAGACCAG |
| 774 | 1382 | CATTGAATGTCTACCATATGCCTG | | TCATTTCATGTGTGTAAATCATGTTATG | P | AGAAGACCTATGCCCTTTACTCAAA | AGAAGACCTATGCCCTTTACTCAAAGAACTTATCTTATTGGCATAACATGA |
| 775 | 1383 | TTGTCTGCAAAGACTGTGAGAGAT | P | TGGCCTTCCTCAGAGATGTG | | GCCAATTTACTTTCTTCTTTTGAAT | ATACACACAACAGAAAAATATGACCCATTCAAAAGAAGAAAGTAAATTGGC |
| 776 | 1384 | AATGGCTTGATCAGAGTTCACTG | | AAAAATAAAAAAATTAGCTGGACATGG | P | CTCCCGGGCTGAAGTGCTCCTCTCA | CTCCCGGGCTGAAGTGCTCCTCTCACGTCACCCTCCTGAGTAGCTGGGACT |
| 777 | 1385 | AAGCCATTAAAGCTGAGAAGAGTTAGT | | AATTTGACCGATAAAAAGACACTCAG | P | ATTGGTTAAGTTCACGCACCTAGAG | ATTGGTTAAGTTCACGCACCTAGAGCGATGGAGCCAGGAACTGTCCTGAGT |
| 778 | 1386 | AATAACATTAGGAGTGTTGGCAGC | P | CATTTCTCCCAAGAGCAGGAA | | TGGGAGCAGAGCAACCTTGTGACGA | CCTGCTCAGAGGGAGGAAGGTGGGACTCGTCACAAGGTTGCTCTGCTCCCA |
| 779 | 1387 | AGGCGGAGGTTGCAGTAAG | P | CTTAATCAGATTGCCTGGTGC | | GGGTAGGGCCCGGAXACAGTATTTTTT | CTCAAACAAAATAAAAATAAAATTTGAAAAAATACTGTATCCGGGCCCTAC |
| 780 | 1388 | CTCATAGAGAAATAGAACACACTCAGCT | P | GGAATCCTAGAACATCACTACATAATTTCT | | TATXTTTAAATTACAAAAXCTACTCCC | CTTACCTCTGAGGAGGGGAGCAGAACGGGAGTAGCTTTTGTAATTTAAAAA |
| 781 | 1389 | TTTTTAGCTCCAGATGACATTAAAAACT | P | GTTAGCCAGGATGGTCTCGAT | | TCGXTCTCCTGACCTCGTGXTCCGTCC | ATCCCGGCACTTTGGGAGGCCGAGGCGGACGGATCACGAGGTCAGGAGATC |
| 782 | 1390 | CCACTGAATTGTACACTCATAAATGG | | ATTTTTTATCTTGTGTTTATACATGTGTGTG | P | AXAATGGXAATTTGGTTTTATATTTGC | AATGGCAATTTGGTTTTATATTTGCGTATATATTTATACAGCTTTTTGTTT |
| 783 | 1391 | ACTCGCAAAAATATAGGTACACATCG | | GGTACCTGTGTCGAAAATCAGTTG | P | TGTAACAGAATAGAAAGCCCAGAAA | TGTAACAGAATAGAAAGCCCAGAAACGGGCCTATGCATGTACAGTCAACTG |
| 784 | 1392 | CAAGAAAACACATTTCCTTATTCACG | P | GTGGAAGGTGTATCTTAAATTGGTCA | | AATTGGTCAAATAAGACXAGATGGAAG | TGCTCTCCCAACCATAAAATATAAGGCTTCCATCTAGTCTTATTTGACCAA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 785 | 1393 | CTAGCAGGCCCAAGAACCTC | | GCATTGATTACATAGGAATACCAGATTT | P | CAAGXCTGTAAGTACAATCTAAAGTCA | AGACTGTAAGTACAATCTAAAGTCAGTCTTGGTTTGGCTTCCTGTCTCAAG |
| 786 | 1396 | TCCTCCATGCCCGACCAC | | CATGAGGGGACTTAGTCTCTGAG | P | TCXCATGTCTTCXGGACCTGAGTTTGG | TCATGTCTTCAGGACCTGAGTTTGGGTTGTGGTGGCCATCCGGACCCCCTC |
| 787 | 1397 | CAGGTCCTCTGAAACCTGGAT | P | AAATGTGACTAAGTCATTACAAATGTGACT | | GTGAXTGAGTCATTACAGTGGACCCTC | AAAACGGATTCTTTTCAATGCACCCGGAGGGTCCACTGTAATGACTCAGTC |
| 788 | 1398 | AAATTTGAATCCAGCCATACCTG | | CTTTTTCTACCTTATGCCCCTCA | P | ATTXACTTTAXCTGTGGTGAATCTGTA | TCACTTTACCTGTGGTGAATCTGTACAGGTCTGCAGCTACCTCAGTTCTTG |
| 789 | 1399 | TACTAGTCTCAGAAGTATTTGTGTTTCAAGAA | | TGTTGGCCCATACCTGCTAA | P | TGAATTGTATTTGGGATTATGGAAA | TGAATTGTATTTGGGATTATGGAAAGYAATGTTTTAATAAGTAAGACATAT |
| 790 | 1400 | TTTCCATGTGTGTGCCTGAG | | GATTTCTTTCTACACAAGGTCACCTG | P | ACCCATCCCCATTGGCTCTTCTACA | ACCCATCCCCATTGGCTCTTCTACAGGTGATGTGTCTACTGTACACCTACA |
| 791 | 1401 | CTGAAGATTTATATTGATATTTGATGGAAAG | P | TGGGCTACAGATCAAGAGCTAGG | | GGAAGAAAATATACCTTTAGAGTTA | ATTCTGGATGCATACAGGTTATATGGTAACTCTAAAGGTATATTTTCTTCC |
| 792 | 1402 | AATATATGTGTGTGTATGCAGTTTAAATTACC | | ACTGAATGGCCTCCTGTGG | P | GCCAAGAACAAGGTGGTTXCAGTTAAG | CAAGAACAAGGTGGTTGCAGTTAAGGTGGTTAAAGCAGGTCTGTGGTGATC |
| 793 | 1403 | GTTTTATAGGATTTGGGTAGATAAAGG | P | CTTCTCCTGGCCCATCCT | | TGTGACCCCCACTCCTGCCCACCAG | AAATTACAGTCAAAGGGGTTTGTTCCCTGGTGGGCAGGAGTGGGGGTCACA |
| 794 | 1404 | TAGGCTCCTGCACTTAGACTCCT | P | CAGTGTCAGATGAGCAGCAGG | | TGGATGTTGTGCAGAGTGGAGAATG | TCATGCTGCATCAGCTCTTGGCCCCACATTCTCCACTCTGCACAACATCCA |
| 795 | 1405 | ACCGGGAGGTGAAGGCCG | | CAGKCTGGGGAAGCTGGG | P | AGCCCCGCTCCCGTCCTTTGATTCT | AGCCCCGCTCCCGTCCTTTGATTCTGTCCCAGCACACGGCACCGGCAGAGC |
| 796 | 1406 | TTTGATTCTKTCCCAGCACAC | P | GGCCTGCCATTCTTCTGTG | | GTGCCGTCGGCXTCGGGAGGATGACAG | ACCGGCAGAGCCCCAGCTTCCCCAGACTGTCATCCTCCCGAGGCCGACGGC |
| 797 | 1407 | GCTTGGCCCAGGAGTTCT | | TTTGACAGCAAAGACACTTCATTC | P | AACCTAACCCATTATTTTGTTGGTC | AACCTAACCCATTATTTTGTTGGTCGAAACAACAGCTACATCATTGAATGA |
| 798 | 1408 | ATGTAGCTGGTCAGTTCATGGTTTA | | GTTTGTGTGTCTGTACACACTCTTCTG | P | TGAGTCATGGAACTCTGGGAGGGTC | TGAGTCATGGAACTCTGGGAGGGTCGAATAAAAGCAAAAATTTCTCTCCTC |
| 799 | 1409 | AGAGATTTGGTGAGGGTTAACATGT | | CATGATCTTCCCATCTCAGCC | P | CATTTAAACXAGAGGCAGTGGCTCAOG | TTTAAACCAGAGGCAGTGGCTCACGACCGTAATCCTAGCTACTTGGGAGGC |
| 800 | 1410 | AGTGTTTGTGTCCCTGGGTACTT | | GAAACATGTGCTGTGTCCACTC | P | AGGGAGTGGTGATGACTCTXAACGAGC | GGAGTGGTGATGACTCTTAACGAGCATGCTGCCTTCAAGCATCTGTTTAAC |
| 801 | 1411 | TAACCTCAATAATAACCATCACTTTAGG | P | CATTTTTGGGCACCATCC | | TGGTGCCAAGCCXTCCAGGTGATTCTG | CAATGTTTAAAAACTTGAGCATGCACCAGAATCACCTGGAGGGCTTGGCAC |
| 802 | 1412 | CTTTGGTGCTTCCAGCTCAG | | ACAAGCAAAAGAGAAAAAAAGCC | P | CTGGTTTTCCATGACCTGAGAGACT | CTGGTTTTCCATGACCTGAGAGACTGTGACCAAAGTTAACTTTTTATCTCT |
| 803 | 1413 | CAGTTATACCTTTTAAATCCTACTGGGC | | GCACTTGCCCCCAAATTT | P | GAATXCACTGTTTCTGGAACATCAAAA | ATCCACTGTTTCTGGAACATCAAAAGAGCAATGGCCTAATTAAGATAAATA |
| 804 | 1414 | CATATGCTAAGTGATCAATCGAAGTTAA | P | AACTCTGGTCTTGGGACATGTTAA | | TGTTAATTAACATCTCTAAGCCTCA | TAATACCATTTTACAAATGATAAAACTGAGGCTTAGAGATGTTAATTAACA |
| 805 | 1415 | AACAACGCTGCGCTGACA | | TTTGAAACTTCACTCGTTCCAGTT | P | ACATCAGGAGGGGCCACGGTGAACA | ACATCAGGAGGGGCCACGGTGAACACAGGAAATGGCTTTGGCAAATACTTG |
| 806 | 1416 | AAGTAGTAGGTGAGGTACTAATTATGGCAG | | AAGAGAAGCAATGACCCCTCA | P | AACTCTTAAACTATTCAGTATCTCA | AACTCTTAAACTATTCAGTATCTCAGTAACCACACTATAGTATATACTGTA |
| 807 | 1417 | CCATATCTGCAAGTTCTGAAGATCA | P | TCACTTCTTAGTTTCTTTTCCACGC | | CGCTTATTTTCATTCATYTTGATAT | GAACACACAGAATGTTTGTTGAATTCATATCAARATGAATGAAAATAAGCG |
| 808 | 1418 | GCTGACTTTGAGGTAGGCAAAG | P | TCCTCTGCTTATTCCTTTCTCTTGT | | ATTGTATTAXAAAATTCTTATAGTGAC | AAAAATGATCTGATACAGCTGAAAACGTCACTATAAGAATTTTATAATACA |
| 809 | 1419 | AATGCAGATTGTGGTCCTTATTACC | P | ACTTTCCAGACTTGAAATTAGGTGACTA | | AGTCACATAAACATTCATCTTCAAA | AATAACAATTACGATATTTATTAAAGTTTGAAGATGAATGTTTATGTGACT |
| 810 | 1420 | AGAAATCTAACTACAAGAGAAATTTGGTGA | | CCATCTCTTCCAGAGACCACC | P | CCTCAGGAGATGTAGAATGGTCACA | CCTCAGGAGATGTAGAATGGTCACAGGCTGCATTTGTATGAGAGTCTGGGT |
| 811 | 1421 | CACCACAGAATGAATTTAGGTGAATAT | | TGGGGTTTATATTAGAATAGGTTTTAGGTT | P | CTGTTGTCCCAGGGCAGTAAAAAAG | CTGTTGTCCCAGGGCAGTAAAAAAGGATACAGGCTACTGAACCTAAAACCT |
| 812 | 1422 | TTTAGGAGGACTCCAGTATTACCTGAT | P | TGACAGGGTAGAGAGCCAACA | | ACAAGTAGGACTTTTCATTTATTTA | GAGAAATCTGCAGAGAYTCTTAACCCTAAATAAATGAAAAGTCCTACTTGT |
| 813 | 1423 | TCAGAACAAACAGTTTAACAAAACCA | | CACCCTGGGCTCAGGACC | P | AGGGGGTTGTGGAGGCAGGGGGCTG | AGGGGGTTGTGGAGGCAGGGGGCTGGGCAGCCTGGAGTGTAAGTGCCAGGG |
| 814 | 1424 | ATCTCTACAAAAAAGACAAATATTAGCTGG | P | GCTCACGGCAGATTTGACC | | ACCTCCCGAATTCAAGTGXTCCTCCCC | TCCCAGCTACTAGGGTGGCTGTGGTGGGGGAGGATCACTTGAATTCGGGAG |
| 815 | 1425 | TACTTATTTATTTCTATCCCAAGCTGTGA | P | CAGTCTATTTTCCCGCCTTTTC | | CTTCCTTTGCCCCTCCCAACTTCCA | GCGGCGATCTGCGACTGCGCRCAGGGTGGAAGTTGGGAGCGGCAAAGGAAG |
| 816 | 1426 | TCAAACTGCATTTTGGTTCACA | P | CAGAACATTGCCAACAACTGG | | AGGAAATGGCGAAATAAAATAAAAT | GTCATCCTTCCTTCTCTTTTTCAAAGATTTTATTTTATTTCGCCATTTCCT |
| 817 | 1427 | CTAAACATAGTTTGGTTCCTTTGTAAGTT | P | TGTACAGATGTTTATCACAGCATTATGTC | | ACAGCATTATGTCXAAGTGGTTTTAGA | TCCAGGTAATGGATGAATGGATTGCCTCTAAAACCACTTAGACATAATGCT |
| 818 | 1428 | TAGCACAGCATCAGTACAGCACTAA | | TCAAAATTAATGCAAAAGTGAACCA | P | TTACCTCAGATATTGTTATTTTGCT | TTACCTCAGATATTGTTATTTTGCTCACATTATTTTGAACGTTATGGTTCA |
| 819 | 1429 | GCAGTAGTGGTTATGTAGCTTTTAATACTATTC | P | TCTTTGTGCCATTTCTTTTTTACC | | ATATGCCTTTCTTTTTAGGGACTTA | TTGCCOMTGGCTCRTTTTAAGATAAGTAAGTCCCTAAAAAGAAAGGCATAT |
| 820 | 1430 | TTTCCTCTCTTTAATGTGATTTCAGC | P | ATAACTCTTCAGAAAATAACAGAAAATGTGA | | GTGAACXGTCAGTTAATACAACAGCCA | TTTCCCAATCTCTTGCTTATGGCTACTGGCTGTTGTATTAACTGACAGTTC |
| 821 | 1431 | ACGAAGATCTCAAAATACTTCAAAACG | P | CTTCAGGTGATGCTCCCG | | TTGGCCTCXCACAGTGCTGGGATTACA | GTCGGCTAGGCACGGTGGCTCATGCCTGTAATCCCAGCACTGTGGGAGGCC |
| 822 | 1433 | AAAGCGAGAGGAGGAGTGG | P | GCAAGAATTGAGGTTGCTGC | | GCTGCTAGTAACCCAGATAACCGTA | CTTCTTAGAGAGAGGTTGGGGTGCAGTACCGTTATCTGGGTTACTAGCAGC |
| 823 | 1434 | ATCTTCTGAGCCCGGAAGTTT | | CCTTAGTTTCCTTAGCTGTCTTTTTATTTTA | P | CXACTXCATTTCAACCTGGGCAACAGA | ACTGCATTTCAACCTGGGCAACAGAGTGAGACCCTGTCTCAAAAAAAATAA |
| 824 | 1435 | TCAACACACTCTATCCCAGCAC | P | CAAAAATGTTTTCCCCACATAAAC | | GAGGGTCAGCAGGTTGGATAATGAG | ACTTCCACGGTGTCACAATTAAACAACTCATTATCCAACCTGCTGACCCTC |
| 825 | 1436 | TACTAAAAATACAAAAGTTAGCCGGG | P | CTCCGCCTCCCAGGTTCA | | AGCGATTCTCCTGCCTCXGCTTCCT | GCAGKTGCCTGTAATCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCGCT |
| 826 | 1437 | GCCTTTATGCCAAATGTCTTAGACTA | | AGACCTCAAAAGCAAAATAATCAGG | P | TTCCAAAAGAAAATAGAGGAGTTAT | TTCCAAAAGAAAATAGAGGAGTTATGGAGACCAATATTTAATAGAATAATG |
| 827 | 1438 | TGTACAAGACAAGGATGCCCA | P | GGATACTCTTTATTTCTTTCTCTTGACTGG | | ATACTATXTTGAATAAGAGTAGTGAAA | TTCCTCTAAGATCTTGTACAAGACAAGGATGCCCACTTTCACTACTC |
| 828 | 1439 | AAAATACTGAGCTGAGAGAGCTGTTC | P | CAAAAAAGGTGCAGATTTTTACCTACT | | AGACCCAGGGTCAGGTGAAGTTCTT | TTGACATCATAGTCCACAGTTTATGAAAGAACTTCACCTGACCCTGGGTCT |
| 829 | 1440 | CATGAGTGGATGCAGGGC | | CATGCAGGGTGTGAAATCCT | P | GAATAAGGAGCAGTGGAATAAAAAA | GAATAAGGAGCAGTGGAATAAAAAAGCAAATGAGCGAGAGTTTATCAACAT |
| 830 | 1441 | AGAAAAGCTGTGATTTTAAAGTTTCCA | P | CTCGGAGGCTGTCAAGATTATG | | ATGTTACACAGTCCCCACAAGTGCT | GGTGAAGCCTAGATACAGAGGTCCACAGCACTTGTGGGGACTGTGTAACAT |
| 831 | 1442 | TAATCAAACAAAATAATCTGGCAGG | | GGCCCCTCTAACACACCTCT | P | CCCACAGGTGAATCATACAGAGTTT | CCCACAGGTGAATCATACAGAGTTTAAAAAATGTTGGTATGTTTAAACCAG |
| 832 | 1443 | ATTATTAAAATCCCCCACGGAAG | | CATTAACAAGACACACAGGGTGG | P | CCCAGXGTTGCCTATCTCCTGACTCCA | CAGAGTTGCCTATCTCCTGACTCCACTGCACTCCCATTTGCCTTCTTTCCC |
| 833 | 1445 | CTTTGGCATAGAGTAGGAGTCAAATATT | P | TTAATGGTACACAAATAAGAAGTCAACAGT | | GAAGTCAACAGTACCAAAACCCATA | CTTAGAGTAATGCTATTTCACAAACATATGGGTTTTGGTACTGTTGACTTC |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| | | | - | | - | | |
| 834 | 1446 | GACAGACTCATCAGATTTAGGAAACC | P | TGAGGCGAGGCTTGGTAA | | GCTAGTGACTGTTTTTTTTTGTTTG | ACAGGCAAAAAAAAAAAAAAACCAAACAAACAAAAAAAAAACAGTCACTAGC |
| 835 | 1447 | AAATAATAAAGCCAGGATCATGAGAA | P | TCAAGAGAATCACGATTAGCCTTTAT | | CTATTGCTTGTATATCTCATTTCAT | ACATTAGGAAAAAACAAGTGAATGGGATGAAATGAGATATACAAGCAATAG |
| 836 | 1448 | TTCAAAGCCCTCTTCCAGTTC | | CAAAGAATCAAGAATCAGTGTGGA | P | GGATGAAATGAGTGTCAGAGCAGGG | GGATGAAATGAGTGTCAGAGCAGGGAATGGAAAGGAGAGTAGAAACTTTAT |
| 837 | 1449 | ATATTTGAAAGAATAAGCAGTATATGTCATTAGG | P | TGTGCCATTTTTGCATTCCT | | GGATTCTGACCATTTCAATAGGTGC | AAATTCAAAAAATGAAATACTATTACGCACCTATTGAAATGGTCAGAATCC |
| 838 | 1450 | AATTTTTTTAGAGAGATATCATAAGGAGCTC | P | AAAATTCAACAGTTCTCAACCATTTC | | ACCATTTCCTTTAGCAATCGCCCAT | TAGTTAATTTCCATCATAGTCTATGCATGGGCGATTGCTAAAGGAAATGGT |
| 839 | 1451 | TGCAGAGCTGGGAGAAAGAA | | GTAGTGGAGATAGTACCTGAACCCC | P | AGTGTGATAGAGTAGTAAGXGCATGGA | TGTGATAGAGTAGTAAGTGCATGGAGTTTTACTTAAGTCAGAAATTGGGGT |
| 840 | 1452 | GTGCGATCTGGGCTCACT | P | CATGCCTGTCATCCCAGC | | TACTGGGGAGGCTGAGGCAGGACAA | AGTCTCTGCCTCCTGAGTTCAAGTGGTTGTCCTGCCTCAGCCTCCCCAGTA |
| 841 | 1454 | ATTGATATTCGCAAGGAAAACACA | P | GTCACTGCTGCTGCCTTCC | | CCTTGGCTAATATGATTCAAAGAGA | TTGCCCTTTCCCCTTGAATTTGGAGGTCTCTTTGAATCATATTAGCCAAGG |
| 842 | 1455 | TTCTAGAGAGGCAGGGCCTAG | P | GACTCAAAGGAAGAGACTCAGGATC | | AGTGAGGACAGACCCAGAAACACAG | TTCCTGGTTTGACCCCTTCCCACCCCCTGTGTTTCTGGGTCTGTCCTCACT |
| 843 | 1456 | CCACACAAGAACATCTACACTACGAT | P | TGCTAACTATTGTATAACCTCTATAACCATGA | | TATAACCATGACTTGTGAGCAGTAA | TTTTGCTCCTGTGATGGTATGTTAGCTTACTGCTCACAAGTCATGGTTATA |
| 844 | 1457 | CTAGCTCGGTACCCTGACCAC | | TGCTTTCTGCTGTAGGGTCTG | P | TTGAATAAGAXTTGCTCACAGAAAAAT | GAATAAGATTTGCTCACAGAAAAATAAGCTTAAATCTACAATGAATGCCAG |
| 845 | 1458 | TTATTGAAGGCCCTGTGGAC | P | CAGGATCTCCCAGGTCCATC | | CATCCXAATATGTGCTTTGTCCACTTT | CCCAGTGATGCCCAAGGGCCTAGTCGAAAGTGGACAAAGCACATATTTGGA |
| 846 | 1460 | TAATGCCAGCTCCTCGGG | | GTATTTATTTAGAGACCGAGTCTCACTCA | P | GCGGGAGAATCGCTTGAACCAGGGA | GCGGGAGAATCGCTTGAACCAGGGAGGCGGAGGCTGCAGGGAGCCGAGATC |
| 847 | 1461 | GTGGCAAAGCCTTCACAACTAG | | AGAAGTGAATGGGAGAAAAATAGAATATG | P | CCATCTGTAGACTGTCAAAXTATGTAT | ATCTGTAGACTGTCAAAATATGTATGTATGTAATTTTGACGTATGAACCTG |
| 848 | 1462 | TTCAGTGAGTTGCGTGAATTC | | GGGCACCCTTATCTTTGACAC | P | TCTAGTGAATTATAAAATCTAAGGA | TCTAGTGAATTATAAAATCTAAGGACGGATTTAGGAATCCCCTTAAATTTG |
| 849 | 1463 | ACCATTGGCAAGAGCTAAAAG | P | GTAGCAGCGCCCAGTTTTC | | ATTGTAGTTCATTTGACCCTCCCCA | TGGACACAAGCCGGATGGCCCGCGGATGGGGAGGGTCAAATGAACTACAAT |
| 850 | 1464 | ATTAACCTCAGCGATTGTTGCT | P | CTATTGAGGAGAGGATGGGAGG | | CCAGGCAGGGCCACCAGGAAGAGCG | ACACCTGGGTGAGTTTGGAGCGCTCGCGCTCTTCCTGGTGGCCCTGCCTGG |
| 851 | 1466 | TTGCAGAGTCTATGTCGATTCTAGAG | | GAATACTGTCGGACACAGCACTG | P | TGAGCAAGATTGTGACATAGGTAAAGTTGTGACGGGGGTGTTTTTTGTGCA | TGAGCAAGATTGTGACATAGGTAAAGTTGTGACGGGGGTGTTTTTTGTGCA |
| 852 | 1467 | AGGCCAAGCTAGTCCACCTC | P | CATCCGGTAATTAGCGATGCTA | | TCCAAGGAACCAATCATXAAAGAACAC | TGGCTTTCCTCTCTTTCTTCCAGCACGTGTTCTTTAATGATTGGTTCCTTG |
| 853 | 1468 | TCATTCCAAGGGTGATGGC | | AAAAAAGAAAGAAAGAAAGAAATTGGC | P | TGTAAGCAAGGGCAGCACTCTGGGT | TGTAAGCAAGGGCAGCACTCTGGGTCCGACGGGGAGAGTGAGCGGGAGAGT |
| 854 | 1469 | AGGAATTCAAAATCTGGACAAAGAC | P | TGTCATTTACTGCCCAGAATAACTG | | AACTGCCCTGXAGATTGCTTTTCTTCC | GGCTCAGGAAAGAAAATTTCAGATGCGGAAGAAAAGCAATCTGCAGGGCAG |
| 855 | 1470 | CTTTAGCTTATACAGTGTGCATGAAGAA | | CAAGCACTTAAAAATTCTCTATTTTACATAAGG | P | AGCACAATGCAAATAGAAAACCGAA | AGCACAATGCAAATAGAAAACCGAAATTTTATTTTCCTCACAAAATTATAT |
| 856 | 1471 | AGGTGCCCACTCATTCTGC | | GGGGAGCCAGCCTCTTCT | P | CCACATGGACCACAAGTGCTGTCTC | CCACATGGACCACAAGTGCTGTCTCGGCTCAGTGTGGTTCCAGAGAACCTG |
| 857 | 1472 | TACTTGGATGGAGCATGTCAAG | | CTACTTTAGGCAGGGACCGAA | P | GTCCATCCATCCTATCAACAAATCT | GTCCATCCATCCTATCAACAAATCTCTAGGAACTTCTACCATGAGCAAGGC |
| 858 | 1473 | TTATGAAAAACCCACAGCCAATAT | P | CATGGATCACCTGTTCCTGG | | AATTCATTCTCCCATTTCTTAGGTT | TGAAAACTGGCACAAGACAGGGATGCAACCTAAGAAATGGGAGAATGAATT |
| 859 | 1474 | TTGCCTATGGTTAGGGTTGTGA | | GTAGCCTTGTCTGTGGGCC | P | AAACCTCAGTGGTGCCAAAXATCAAAA | ACCTCAGTGGTGCCAAAGATCAAAAAGGGTTATTTGGGAAAAGCATGCCCT |
| 860 | 1475 | CTTTGATGTTTATTGATATGACACCG | | AGTACCAGATTTTCAAGTTACATAAGTGAAC | P | TGTTTAAACAACGCAAGTATGTCCA | TGTTTAAACAACGCAAGTATGTCCACGTGTTTCTTATAGGGTACACTTGAA |
| 861 | 1476 | ACGTCTTAAGCACCTTTCTGCA | P | AAGTGACAGGATTCAGAAGCCA | | TATCAGAAAAATCCATCAGGXCTCAGC | TCCCTACAACACTTTCTGTTGCTTGGGCTGAGCCCTGATGGATTTTTCTGA |
| 862 | 1477 | TGGAGGCCCAGAGGACGC | | GAAACTGAGTCTGGATAGGGGTAAG | P | AGGGACAXGATCTCTGTGATTTCCTAA | GGACAGGATCTCTGTGATTTCCTAACGGGGACATCCCCAGGCTCCTCTTAC |
| 863 | 1478 | TGTGGTGAGCCAAGATAGCTACA | P | CCTTCCCAATTAAAAGCAGCTAAT | | TTGATGTTCAGATTTTCCTTTTTTT | AAGAGTGAAATTCTGTCTCAGAAAAAAAAAAAAGGAAAATCTGAACATCAA |
| 864 | 1479 | TTTAGCTTTGGGCAGTCGAC | P | GGCCAGCAGCTTGTGGAT | | GTGCCCGGGATGCCTGTATCTATGC | GTTTCTGTCTACTCCAACGTCCACGGGCATAGATACAGGCATCCCGGGCAC |
| 865 | 1480 | CTCATAAATTTCCATATTGTTTCTCTGTACT | | AGGAAAAACTGCCTCACCAAA | P | GTTGAAGTGCACAGATTTTTTTTTT | GTTGAAGTGCACAGATTTTTTTTTTAAAAAAAACAGCTATTTGAATTTTTT |
| 866 | 1481 | TGATGGACAGGGCCATAAAG | P | CTCACCTAACCCTGCCCC | | CTGACAGTATTTCTCCACCCGCCCT | GTTTATGGTTTTTGTGATCAGCTACCAGGGCGGGTGGAGAAATACTGTCAG |
| 867 | 1482 | ATCCTGTTAACTCAGGAGCTGACC | P | CTTTATTTTCCCACCTGTTAGACATTC | | ACAGXGATTTGGCCAGTTGTATTTCAC | GGAAAACACTATCTAGTTCCATTACCGTGAAATACAACTGGCCAAATCACT |
| 868 | 1483 | TTTTTGAATGTTTTGGCCCA | | GGAAGCAGGAAAAAGGTCCC | P | ATGGCXGGCAGXTTCCAGCATAAGTCA | GGCTGGCAGCTTCCAGCATAAGTCAAGCTCCCCATCCCCCAGGGGACATGG |
| 869 | 1486 | AATTCTAGCTCGGTACCCGG | | CATTTTACTTGAACACAGACCGAAG | P | TTAAATCTGAGTGXAACATCCGTAGAA | AAATCTGAGTGGAACATCCGTAGAAGTAGCTCACAGACAATGCAGAAGTAG |
| 870 | 1487 | GCAGGTGTTCTGACTCAGCC | | CTTAAACCAGAACTGCCTAGCAAA | P | CTTTGATGXACACACTGCTGCTCATTC | TTGATGCACACACTGCTGCTCATTCAATCTAGGGGCAAGTCTCATTTTGCT |
| 871 | 1488 | CCATTCACAGATGCAGTAGAGTGA | | AAATACTTGATAATTCTTGGACTTTCTCTTT | P | ACTGTTCTAAGATTGAAACTAAACC | ACTGTTCTAAGATTGAAACTAAACCGTACTGGGTTTGAAAAGAGAAAGTCC |
| 872 | 1489 | CAACACAGTAACATATTCATGAGTTTTTAAA | | CAGGCTGAGACAACCCATCA | P | CACTTGGTGATCTCTGACAATGTTA | CACTTGGTGATCTCTGACAATGTTACGTAGCCTGAACCTGGAGTTTTGGCT |
| 873 | 1490 | TCTCTTGCCTTAAATCTAGAGACAATCT | P | CAGGTGGAACAGTGGAAGCA | | AGCGACAAGAATGTAGACAGGCTAC | AGGGATAACTCTGAAGAACAGAATACGTAGCCTGTCTACATTCTTGTCGCT |
| 874 | 1491 | TGCACAACAGAAGGAAAGGTG | | CCTCTCTACACTTACCGTTTCTGC | P | TCATTCATCCACCTTTTCCTGTCTC | TCATTCATCCACCTTTTCCTGTCTCCGGCGTGTGCGATGCTCCCGCGTGTGG |
| 875 | 1492 | TCTTAGAAAGTGATCTTTGGGAATATAGG | P | GAAATCTTCTATCTAGTCATGCCTCAGT | | GTCTTCTTCTCTAAATGCTTCCTCT | TTGACATGTGGAAGAACTCTGTTTCGAGAGGAAGCATTTAGAGAAGAAGAC |
| 876 | 1493 | TTGTCTAAGTGCTCCTTGTAGAGAAG | | CAGAGACGCCTCGGCTAG | P | CAGXACTGACGAAGATGCGGACAAAGC | GCACTGACGAAGATGCGGACAAAGCGGGGGGAAGGACACCCCTGCCTTTGTG |
| 877 | 1494 | AAGGTGGTTAGCCTGGGG | P | CCAGCCTTGCTGTGGGAG | | GTCTTTGGAGGGAATGAGTAGAGCC | CTTCTCCAGAGGCAGATGAGACTTCCGGCTCTACTCATTCCCTCCAAAGAC |
| 878 | 1496 | CTCCCCAAGGTCGTGAATT | P | ATGGTGGGTGTAGGTGCGT | | GTTTTCTCCCACCCCGTCCXGCTCTAG | AGGCTGCCCTGGAGAACTGGAAGCCGCTAGAGCTGGACGGGGTGGGAGAAA |
| 879 | 1497 | ATACACACACATCTACCCCAAGGA | | CATCTGGGCTGATGGTGC | P | GACCAGATAAACACAXGTXGCCATCTT | CCAGATAAACACACGTGGCCATCTTGGACCATGGGGCAGCCAACAATGTGA |
| 880 | 1498 | GAGAGTTTTACTTCTTCCTTTTTGGTCTA | P | AGATTCTGGTGGCAGAAAGACA | | GACAAAAACGTACATTCATTTATTC | TGCCACTTACATTTCTATGTATGTACGAATAAATGAATGTACGTTTTTGTC |
| 881 | 1499 | AAGAGTATGTTGAGACAGCAATAAGAG | P | TCCTGATCTAGGTTCTGGGATC | | CCTAACTTCTCTCAGCCCCGTCTTC | ATAGATGCACCCACCTGGCAGTGGACGAAGACGGGGCTGAGAGAAGTTAGG |
| 882 | 1500 | TGGAGGAAGAGGTATTTAAGGTTTG | | CCAGGTGTCAAAAACCTATACTATAATCTC | P | TAAGATCATATAGGGGGCTGGACGC | TAAGATCATATAGGGGGCTGGACGCGAAGATCTGAACCTGAGATTATAGTA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 883 | 1501 | CGTGGTGGCTCACACCTG | P | CTAATTTTTGTATTTTTAGTAGAGACGGGG | | ACTCCTGACCTCAAGTGATACACCC | ATCCCAGCACTTTGTGAGGCCGAGGCGGGTGTATCACTTGAGGTCAGGAGT |
| 884 | 1502 | AAAGCAAAAAACAACAAACGATC | | CAGAGGGCTTTGGATGCA | P | CAGAAAGGTCAAXTGCCTCACTCAAGG | GAAAGGTCAAGTGCCTCACTCAAGGCCACACAGCTAGCACTCAGGTCTGGC |
| 885 | 1503 | GGTTGAAACAAATCAAAACAAAAAAG | P | ACCGTAACTGGGAGTCACCTG | | CAATGTTACAAGCTCAAGCATGGTA | CTCCTTGGAGCTGTCCTAAATTCATATACCATGCTTGAGCTTGTAACATTG |
| 886 | 1504 | CCTGCCTCAGACAACACAGC | P | GTGGCTTGGGGATTTGTG | | GGCCACCGGCCACAXCTCACCCAGC | GACAGACGAACATCTGTTAAAACTCCGCTGGGTGAGCTGTGGCCGGTGGCC |
| 887 | 1505 | ATTAGGACTTATCCCTGTGCCAA | P | CAAATAATATAAGAGCTCCTGAGTGGG | | ATATCTCTAGAGCACATTTCAAAGT | GCTACAACTTTGTTGCTTCGAGTTTGACTTTGAAATGTGCTCTAGAGATAT |
| 888 | 1506 | GCTGAGTGTATTTGTATGGGTCTATTTC | P | TCAGGTGACTGACACTATTCAATTTC | | TAAAACAGTGTAGTXTTGGAGAAATAA | TTCTGTTTTAGTGATCTATTCGTCTATTATTTCTCCAATACTACACTGTTT |
| 889 | 1507 | GGAGTCTTTCCTGTTGGTCAAGT | | AGTTGAGGCTTGATAGGTATTTATTGAAT | P | TCTGGGTTTGACTACTCATTCATTC | TCTGGGTTTGACTACTCATTCATTCGTTTGATCTTTCATTCATTCAATAAA |
| 890 | 1508 | CCTTCGGAACCTTTCAACACA | P | TGAGCTAGAAAAGTAAATGTGTCAGTCC | | GTCAGTCCTTGGTAGCXAAGTTTGTAC | AGAGGATTTGGATAAAATTTATAAACGTACAAACTTTGCTACCAAGGACTG |
| 891 | 1509 | CCCAAGGTGCTCTAAGGCA | P | GATAATGTGCTTTCAGGAAAAACAA | | CTTGXGCAAGTCAGTAACCCTGAGTGT | GCCCCGTTTTACAGAGGAGGCAATTGACACTCAGGGTTACTGACTTGCCCA |
| 892 | 1510 | CAATGGATTTCAGGCTTCTTAGG | | TCTGAGTTTGGCAAAGAAAGTACC | P | AGAGCTTTCATCATGGCAAGACATC | AGAGCTTTCATCATGGCAAGACATCGACTCTTTTGAGGAAATTCCAAAGGT |
| 893 | 1511 | CCAGTGGCTCATCTCGTGG | P | GTCTGATTTCTGGTGTTGGGG | | GACAAGGTTTCTAGAGGTAATCACT | CAGCGGCTCATTCTAAATGTAATGTGAGTGATTACCTCTAGAAACCTTGTC |
| 894 | 1512 | GCAGTCTGAGAGATATGGATGACATAT | P | AGTTAGGTTCATTTGTTTCATTTTCCT | | TTCTTTTTGACTTTTTATCATTGTA | GACTCGGGAATCATGTAAGTTTCTTCTACAATGATAAAAAGTCAAAAAGAA |
| 895 | 1513 | ATTCAAGCACGAGAAGCCC | P | CAATAGGTGAAGAGGGCCTCC | | TGAAGGTCATACAACCAGAACCCAC | TGGGCACTGGGAGGAAGCTGCAACACGTGGGTTCTGGTTGTATGACCTTCA |
| 896 | 1514 | TTTATTCCCATCTTCTTATTCATAACTCG | P | ATTGGAGCCAGGAGAGCAC | | ACAGAGAGAGAACCTAATCCXGCACGG | GCCGGACGATGATGCCGCTGCTAGAACCGTGCGGGATTAGGTTCTCTCTCT |
| 897 | 1515 | ATCAACAACATCCCCTCCTCA | | GTACAGATGGGGGGTCATGA | P | CCCCGTCACCCACCTCACTGTCCTC | CCCCGTCACCCACCTCACTGTCCTCCTCATCCCTATTATCTGGGAGGTCCT |
| 898 | 1516 | GAGTAGTAAGGAGTTTAGAAGCGTACAAAC | | CTGACCCTCGATTGGTTTCC | P | GCTCTGTACTCACATTGGATTTTTG | GCTCTGTACTCACATTGGATTTTTGAGAGACCTTGAGGGTGGGAGCTTTTG |
| 899 | 1517 | TTTTCCAGTCTGAAACATAAAGGAA | P | GCCCACCTTGGCCTCCCA | | AAGTGCTGGGATTACAGGCGTGAGC | AAAATGCTATTGGACCGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTT |
| 900 | 1518 | CAAATACGTGTTAATACGACCATGA | P | CGCCTCCGCCTCCCAAAG | | AGTGCTGAAATTACAGXCGTGAGCCAC | TAAAAGGCCCTTCCTGGCCGGGCGCGGTGGCTCACGCCTGTAATTTCAGCA |
| 901 | 1519 | TCCGTGGCAAAGACATAACTAAG | P | GTTGCTGTGAAAAGAAAGTAAATGAGA | | AAATGAGACAGAGGAGCCCAGCACT | CCCGCATGTGACCTCCCCCAGGGCGGAGTGCTGGGCTCCTCTGTCTCATTT |
| 902 | 1520 | GAAGGCTTCCCTGAGCCTG | P | GTGCCACTTGTAAGCGTGAAC | | TGTCCGTCTCCTCTTCAGCAAAATG | CCCTCATTTGTGCTCGTGAAATGTCGCATTTTGCTGAAGAGGAGACGGACA |
| 903 | 1522 | CTGTTTTCAGGATTATCCAGCAG | P | TCCTGGGTCAAGAAAAGTCTG | | GTTCGAAAATGTGTCAGTAAGTGTG | CGTTATTTAAGAAATCGTGATGGAAGCACACTTACTGACACATTTTCGAAC |
| 904 | 1523 | GCGCATCATTGCCCTTTC | P | CTTACTTTCTCCATTTACCTTAGAGGGA | | AATCACTTACATTAACAAGAGACTC | ATTACAGACTTCACATCAAGTTCAACGAGTCTCTTGTTAATGTAAGTGATT |
| 905 | 1524 | AATATTCACCAGCCCTGCC | P | GGCCTGAGGGAGGCAAAG | | AGGCACTCTCTAXGTGGCAACATCTCA | TCTTATGGGGTTAGAAAAAGCTATCCTGAGATGTTGCCACATAGAGAGTGC |
| 906 | 1525 | TAATCCTTTTCTGCCCCACTG | P | CATGTTCTTTTTGTGATGATGGC | | CAAXATTCTATCATACAACATCTGCTC | TGGCGTGACTTTGGCCAATTGAATGGGAGCAGATGTTGTATGATAGAATCT |
| 907 | 1527 | AAATACTGATTTTAATGGTTTGTGATGC | | CTTCCTGTTCAACCTGTACCATATG | P | CCAGGATCAAAAACTCCACAGGTGA | CCAGGATCAAAAACTCCACAGGTGAGCTGCATAGGCAGCCAAGATTTAGAA |
| 908 | 1528 | CGCACACTCGGGACCCAA | | GTACAGACGCCCCTGCTG | P | CTCCCAGGGATXTCCCAGCGTGAGAGC | CCCAGGGATCTCCCAGCGTGAGAGCAGGGACGGGACTGCGCCGTCACACCT |
| 909 | 1529 | TAAACAAAGATGCAATTTACTACCAGG | | CTCCCCTGTGCCCAAGGT | P | CCAAGGGGGGGGGGAAAACTTCAAC | CCAAGGGGGGGGGGAAAACTTCAACGGTTCTCAGAAGGGGCCTTTCCAACT |
| 910 | 1530 | AACCCACATCTATGACATGATTACG | | GTCTTTTGACACCTATACGTCTAAGGG | P | ATGTAAGGGTTTTTTGACTTTCTAT | ATGTAAGGGTTTTTTGACTTTCTATGTGCTGACTTCATAAGATGTCACTCC |
| 911 | 1531 | AGACTCCCTGGGGCTAATTT | P | GAACTTGTTGATGTGTCTGTGGAA | | AACACATGAAGATCCCAAGGXTCAGCA | GGTGTCACCACTGACTTCCTTGAGGGTGCTGAGCCTTGGGATCTTCATGTG |
| 912 | 1532 | GGAAAGAGATGGTGTGGGG | P | TGAGCAAGGTCATTGTAATACAGAAG | | TAGACGAATAATAAAGGTAAAGGTT | ATTATTACAGGAAAATTTTAACCGAGAACCTTTACCTTTATTATTCGTCTA |
| 913 | 1533 | TGACCCCATCTATGACATCATTAC | P | CAGGAGGGAAAGAGATGAACATT | | CATTCATGGGGTCCTTACAGCAGAT | AACTGTAAAAATAAGGACATTACTACATCTGCTGTAAGGACCCCATGAATG |
| 914 | 1534 | TGCTTGTTGGCATGAGCA | | CACAATCGCCAGGAACACA | P | TGCACATAAAAGCCAAGACTCACTT | TGCACATAAAAGCCAAGACTCACTTCCTTTGGGACAAGTCAGAAAAATCCT |
| 915 | 1535 | AGCTTGACTCTATTTTAGCACTATTTG | | CTGCTATGGCTCTGGCACTAG | P | CTTGACTCTATTTTAGCACTATTTG | CTTGACTCTATTTTAGCACTATTTGGGGTGGAAATGGCAACCCATCCTTCC |
| 916 | 1536 | TGAACAGCATGACATGATTACGA | | CAGTGAGCTGAGATCACCAGC | P | TTCGAGCTCGGTACCCCTGCCTCAT | TTCGAGCTCGGTACCCCTGCCTCATGAAGGCCTTTTCTTCTTCTTTTTTTT |
| 917 | 1537 | CTGTAGCCAAGCAGGGGTT | P | GATTCATGATGGGAAAACATCAA | | TGCCATCTTCTCACCACCCCAAACA | AGCAGCCTGCAGCTTCAACAAGGACGTGTTTGGGGTGGTCAGAAGATGGCA |
| 918 | 1538 | AGGGGGCGTCTGCTCTCA | P | CTCCAGGAGCTGTGGGGA | | TGAAGGACACCCTGAGCGGAAGTG | GACCCTATAGAAGGCTCAGCTTCCCCCACTTCCGCTCAGGGTGTCCCTTCA |
| 919 | 1539 | TCTCAGGAGTCAAAGCGCAT | | CACACTGAGAACCTCGCTCTG | P | TTACCTGTGTTAAAAGCAAGACTCT | TTACCTGTGTTAAAAGCAAGACTCTGCATGCTTATTCTCACATCAGTCAGA |
| 920 | 1541 | TTCTTTAATTCCAGGAAACAATATTCC | | GTTTCCAGGTGACAGGCAAA | P | ACCTGCTXAAGTTATTCAAACTAGCCA | CTGCTGAAGTTATTCAAACTAGCCAATCCTAAGCCTGCTTACTTGGCTTGG |
| 921 | 1542 | CTGGCCTCATGACCTTTTTTAA | P | CTCATGACATTTTTCCCCACAT | | ACTACCATTCACCAGATTATCCCCC | GTGTGAGTTATCCCATTGTACATGGCGGGGGATAATCTGGTGAATGGTAGT |
| 922 | 1543 | AATGTAGGAGTCACCTCCTCCT | | CTTTCTGGGGATGGGGAG | P | CTGTCCCTGTTTCCTCATCCCCACC | CTGTCCCTGTTTCCTCATCCCCACCCCCTTCTCAGCCACCCCACAACACAGC |
| 923 | 1544 | TGGGTCCCCTGAATTTATAATGA | P | AGTGCCTCTCTCAATAGTTGGCT | | CACXGTATCCAACGCAAAGCAAGACTG | ATAAATAATAATAGCTAATATTTATCCAGTCTTGCTTTGCGTTGGATACTG |
| 924 | 1545 | ATCTCTACTAAAAATACAAAAGTAGCCAGG | P | CAATCTCGGCTCACCGCA | | CCTCCCGGGTTAGAGCGATTCTCCT | AGTCCAGCTACTCAGGAGGCTGAGGGAGGAGAATCGCTCTAACCCGGGAGG |
| 925 | 1546 | ATATGGGTTTTCATTTTTAAGATTGGT | P | CGTTGCCTCCAGGAGAAAG | | AAGGCGTGCTGGCGTGAGXCCACAGTC | GGTCCAGGGAGCTGCCCGGCATTGCGGACTGTGGCCTCACGCCAGCACGCC |
| 926 | 1547 | TTTTAGTTTTAAAGCTGAGAAAGCCC | P | TTGTCAAATGGGTAGGTTACTCAAA | | TACTCAAAATTXCATAGTGGGACTGAA | CAGAGCATGCTGTTGGCCAGGGATAATTCAGTCCCACTATGAAATTTTGAG |
| 927 | 1548 | GATTTCTAGCCTCCAGAATTGTGA | | AATGTCTTTGTCCTTTTTGGGC | P | AAATGTTTGTTGTTCAAXCTACATAGT | ATGTTTGTTGTTCAAGCTACATAGTCGATAGAACGTTTGTTATAGTAGCCC |
| 928 | 1549 | GTGGTGGCTTCTGTCTTAGGTC | | GTAATGGAAAAGGCCCAGGA | P | CTCTCTCTTCCAGTGATTTCTCATA | CTCTCTCTTCCAGTGATTTCTCATACTTTGAGGGACACTCTGGCCTGCTTT |
| 929 | 1550 | TGTCTCAACTTTTCCATTTCTGC | P | TGTCCACTCACCTGCTCCG | | CCGACXCCCAAACCGCTAAGGAGAATT | AATCCAGGCACAGGCTGGACCCTCAGAATTCTCCTTAGCGGTTTGGGAGTC |
| 930 | 1551 | TCAGTGCACCCACATGCC | | CGAAGTGCTTGGTGAAGGG | P | GTAGTGGGTGCTCTGGAAGTACCGC | GTAGTGGGTGCTCTGGAAGTACCGCCAACATTGACCTGCATAAGGGTCTAC |
| 931 | 1552 | GAATTGGTCCTTTCACAGCATC | | TGTGGTGTTTATGTAGTATCCTTTTTCC | P | CAGATCTAAACTTTTCXTACAAGGTTA | GATCTAAACTTTTCCTACAAGGTTAGGTACCAAAGGAAGAGCATTAGAGGA |

| Row# | REF# | 1 Upper PCR primer | Modified | 2 Lower PCR primer | Modified | 3 GBA primer | 4 Flanking sequence |
|---|---|---|---|---|---|---|---|
| 932 | 1553 | CCCAGGAGAGACAGTCAGGA | P | TTAAACATTAACCAGCTCCTTCCTC | | AGCXCACAGAGGAGAAGCGGAGACTCA | ACTGGGAGGGCCAGGAGAGGCCTACGTGAGTCTCCGCTTCTCCTCTGTGCG |
| 933 | 1554 | TGCTTCTGCCCCCACAGG | | CATGACAGTTTTCTGGAGGCC | P | TATCAGAGGAGXTGGCTTTTCACACCA | TCAGAGGAGGTGGCTTTTCACACCAGGGCAATATTTTTAATCAAGAGTGTG |
| 934 | 1555 | TTGCCTCCCTGGGTGGGC | P | CACACTCCCATGCAGGAGT | | TGACAGAGCAGTGAGCCAAAACCCC | TCAAAACATGAGCTTTTCCAGGGGTGGGGGTTTTGGCTCACTGCTCTGTCA |
| 935 | 1556 | AAGCCTCAACTATATACTGTGCTCTG | | GATTTCATTTCCATCTCTTTTCCTAG | P | GTGGATATATTGAATXCAAAATCAGGC | GGATATATTGAATGCAAAATCAGGCGTGGCCCTTGCCCTCATAGAGCCTAG |

While the invention has been described in detail with reference to certain preferred embodiments thereof, it will be understood that modifications and variations are within the spirit and scope of that which is described and claimed.

We claim:

1. An oligonucleotide comprising a nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, or complementary sequences thereof, wherein n=0 through 934.

2. The oligonucleotide of claim 1, wherein X, when present in said oligonucleotide, corresponds to a single-nucleotide-spacer selected from the group consisting of anucleosidic moieties, abasic moieties, non-naturally occurring nucleotide analogs, and non-Watson/Crick base moieties.

3. An oligonucleotide comprising a nucleic acid that hybridizes with a first portion of nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+4, or complementary sequences thereof, wherein said first portion to which said oligonucleotide hybridizes also hybridizes with a nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, and wherein said oligonucleotide does not hybridize with a nucleotide base on said SEQ ID NO:4n+4, or complementary sequences thereof, corresponding to the nucleotide immediately adjacent the 3' end of said SEQ ID NO:4n+3, wherein n=0 through 934 and n is the same value for both SEQ ID NO:4n+4 and SEQ ID NO:4n+3.

4. An oligonucleotide comprising a nucleic acid that hybridizes with a first portion of nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+4, or complementary sequences thereof, wherein said oligonucleotide does not hybridize with a second portion of said SEQ ID NO:4n+4, or complementary sequences thereof, wherein said second portion of said

SEQ ID NO:4n+4, or complementary sequences thereof, hybridizes with a nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, and wherein said second portion of said SEQ ID NO:4n+4, or complementary sequences thereof, also includes a nucleotide base on said SEQ ID NO:4n+4, or its complement thereof, corresponding to the nucleotide immediately adjacent the 3' end of said SEQ ID NO:4n+3, wherein n=0 through 934 and n is the same value for both SEQ ID NO:4n+4 and SEQ ID NO:4n+3.

5. An oligonucleotide comprising a first portion of nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+4, or complementary sequences thereof, wherein said oligonucleotide excludes a second portion of said SEQ ID NO:4n+4, or complementary sequences thereof, wherein said second portion of said SEQ ID NO:4n+4, or complementary sequences thereof, hybridizes with a nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, and wherein said second portion of said SEQ ID NO:4n+4, or complementary sequences thereof, also includes a nucleotide base on said SEQ ID NO:4n+4, or its complement thereof, corresponding to the nucleotide immediately adjacent the 3' end of said SEQ ID NO:4n+3, wherein n=0 through 934 and n is the same value for both SEQ ID NO:4n+4 and SEQ ID NO:4n+3.

6. An oligonucleotide comprising a nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+1, or complementary sequences thereof, wherein n=0 through 934.

7. An oligonucleotide comprising a nucleic acid sequence selected from the group of SEQ ID NOs

consisting of SEQ ID NO:4n+2, or complementary sequences thereof, wherein n=0 through 934.

8. A pair of oligonucleotides comprising two nucleic acids selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+1 and SEQ ID NO:4n+2, or complementary sequences thereof, wherein n=0 through 934, and wherein said primers correspond to two consecutive SEQ ID NOs having the same value for n.

9. A triplet of oligonucleotides comprising a nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+1, SEQ ID NO:4n+2 and SEQ ID NO:4n+3, or complementary sequences thereof, wherein n=0 through 934, and wherein said oligonucleotides correspond to three consecutive SEQ ID NOs having the same value for n.

10. A kit comprising at least one oligonucleotide of claims 1, 3, 4 or 5.

11. The kit of claim 10, further comprising two amplification primers.

12. The kit of claim 11, wherein said primers comprise a nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+1 and SEQ ID NO:SEQ ID NO:4n+2, or complementary sequences thereof, wherein n=0 through 934, and wherein said three oligonucleotides correspond to three consecutive SEQ ID Nos having the same value for n.

13. A kit comprising an oligonucleotide, wherein said oligonucleotide comprises a nucleic acid sequence selected from the group of SEQ ID NOs consisting

of SEQ ID NO:4n+3, or complementary sequences thereof, wherein n=0 through 934.

14. The kit of claim 13, further comprising two amplification primers.

15. The kit of claim 14, wherein said primers comprise a nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+1 and SEQ ID NO:4n+2, or complementary sequences thereof, wherein n=0 through 934, and wherein said three oligonucleotides correspond to three consecutive SEQ ID NOs having the same value for n.

16. A kit comprising the two oligonucleotides of claim 8.

17. A kit comprising the three oligonucleotides of claim 9.

18. A method of genotyping a nucleic acid sample comprising hybridizing the oligonucleotide of claims 1, 3, 4 or 5 to the nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+4, or complementary sequences thereof.

19. The method of claim 18, wherein said oligonucleotide is employed in a primer extension reaction.

20. The method of claim 19, wherein said primer extension reaction is a single-nucleotide primer extension.

21. A method of genotyping a nucleic acid sample comprising performing a primer extension reaction employing the oligonucleotide of claims 1, 3, 4 or 5.

22. The method of claim 18, wherein said primer extension reaction is a single-nucleotide primer extension.

23. A method of genotyping a nucleic acid sample comprising performing a primer extension reaction employing an oligonucleotide comprising a nucleic acid, or fragment thereof, selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, or complementary sequences thereof, wherein n=0 through 934.

24. The method of claim 23, wherein said primer extension reaction is a single-nucleotide primer extension.

25. The method of claim 23, wherein said fragment excludes from 1 up to 10 nucleotides from the 3' end of said SEQ ID NO:4n+3.

26. A fragment of SEQ ID NO:4n+3, wherein n=0 through 934, wherein said fragment excludes from 1 up to 10 nucleotides from the 3' end of said SEQ ID NO:4n+3.

27. A method of genotyping a nucleic acid sample comprising:

a) amplifying a target nucleic acid sequence that hybridizes to an oligonucleotide selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, or complementary sequences thereof; and

b) performing a single-nucleotide primer extension reaction employing an oligonucleotide comprising a nucleic acid selected from the group of SEQ ID NOs consisting of SEQ ID NO:4n+3, or complementary sequences thereof,

wherein n=0 through 934 and is the same value in both steps a and b.

28. A mixture of reagents comprising:
(a) 10 to 200 mM buffer, having a pH ranging from 6.0 to 9.0;
(b) 15 to 250 mM monovalent-cation salt;
(c) 0.5 to 25 mM divalent-cation salt;
(d) 0 to 0.02% volume exclusion agent
(e) 0.25 to 2.5 mM of each of dATP, dCTP, dGTP and dTTP.

29. A method of amplifying a nucleic acid sample comprising the steps of:

(a) combining two amplification oligonucleotides with said nucleic acid sample;
(b) adding to said nucleic acid a reagent comprising:

(i) 10 to 200 mM buffer, having a pH ranging from 6.0 to 9.0;
(ii) 15 to 250 mM monovalent-cation salt;
(iii) 0.5 to 25 mM divalent-cation salt;
(iv) 0 to 0.02% volume exclusion agent
(v) 0.25 to 2.5 mM of each of dATP, dCTP, dGTP and dTTP.

(c) contacting said nucleic acid with a nucleic acid polymerase.

30. An oligonucleotide comprising a nucleic acid sequence selected from the group of SEQ ID NOs consisting of SEQ ID NOs: 1-3740, or complementary sequences thereof.

# Diagram of GBA Process

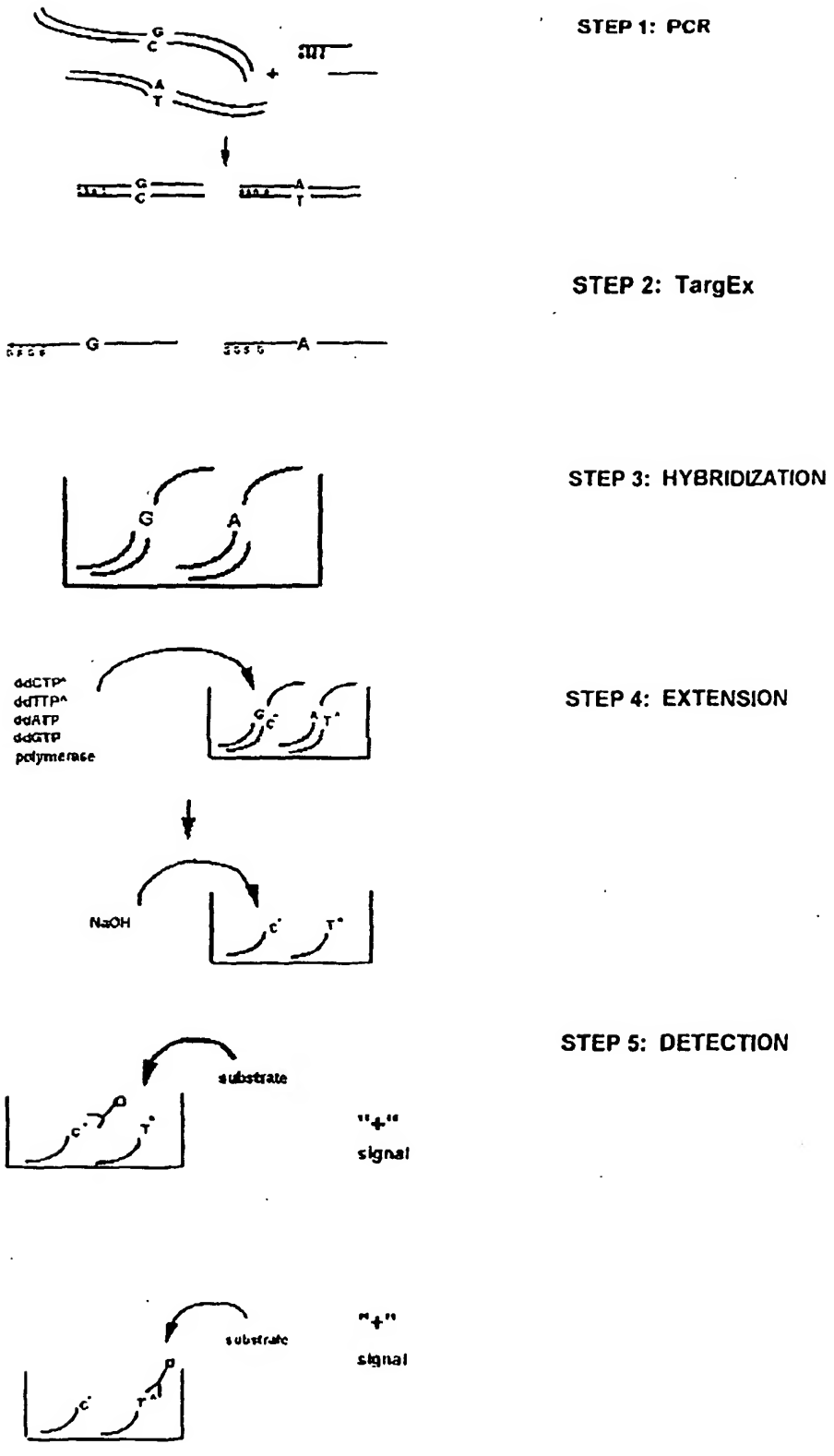


Figure 1

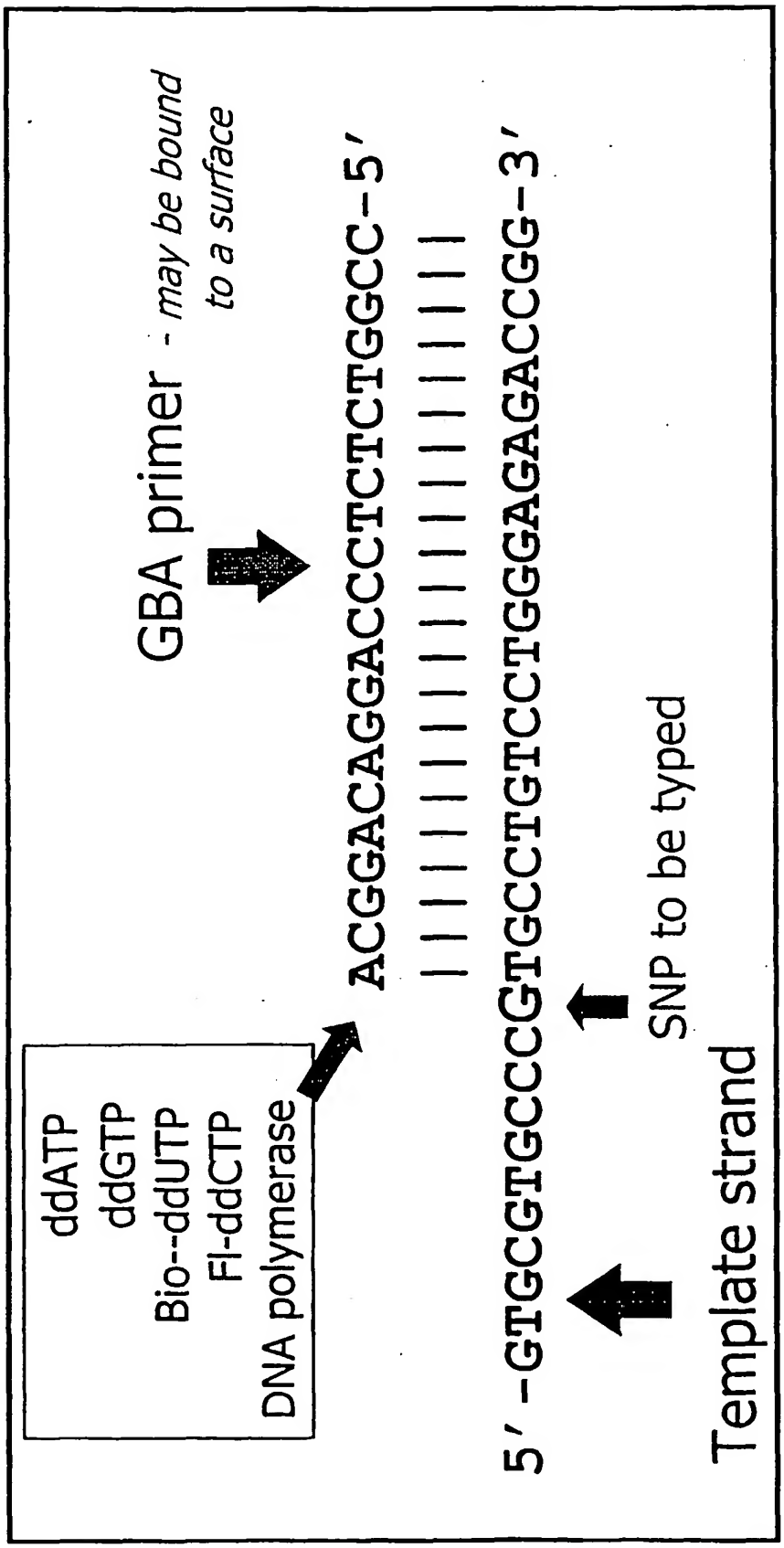
GBA primer - may be bound to a surface
ACGGACAGGACCCTCTCTGGCC-5′
5′-GTGCGTGCCCGTGCCTGTCCTGGGAGACCGG-3′
SNP to be typed
Template strand
ddATP
ddGTP
Bio--ddUTP
Fl-ddCTP
DNA polymerase

FIGURE 2A

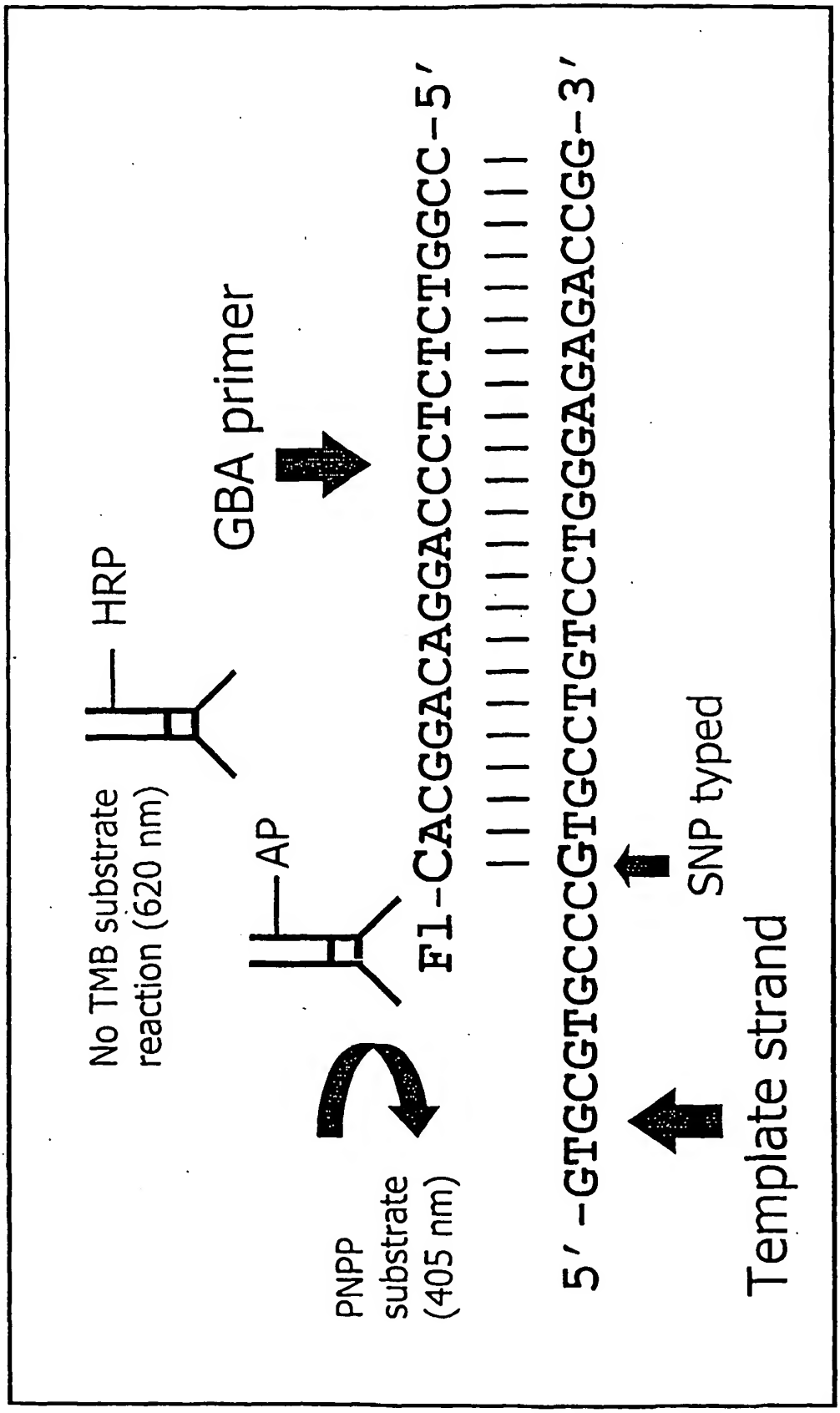
HRP
No TMB substrate reaction (620 nm)
GBA primer
AP
F1-CACGGACAGGACCCTCTCTGGCC-5′
PNPP substrate (405 nm)
5′-GTGCGTGCCCGTGCCTGTCCTGGGAGACCGG-3′
SNP typed
Template strand

FIGURE 2B

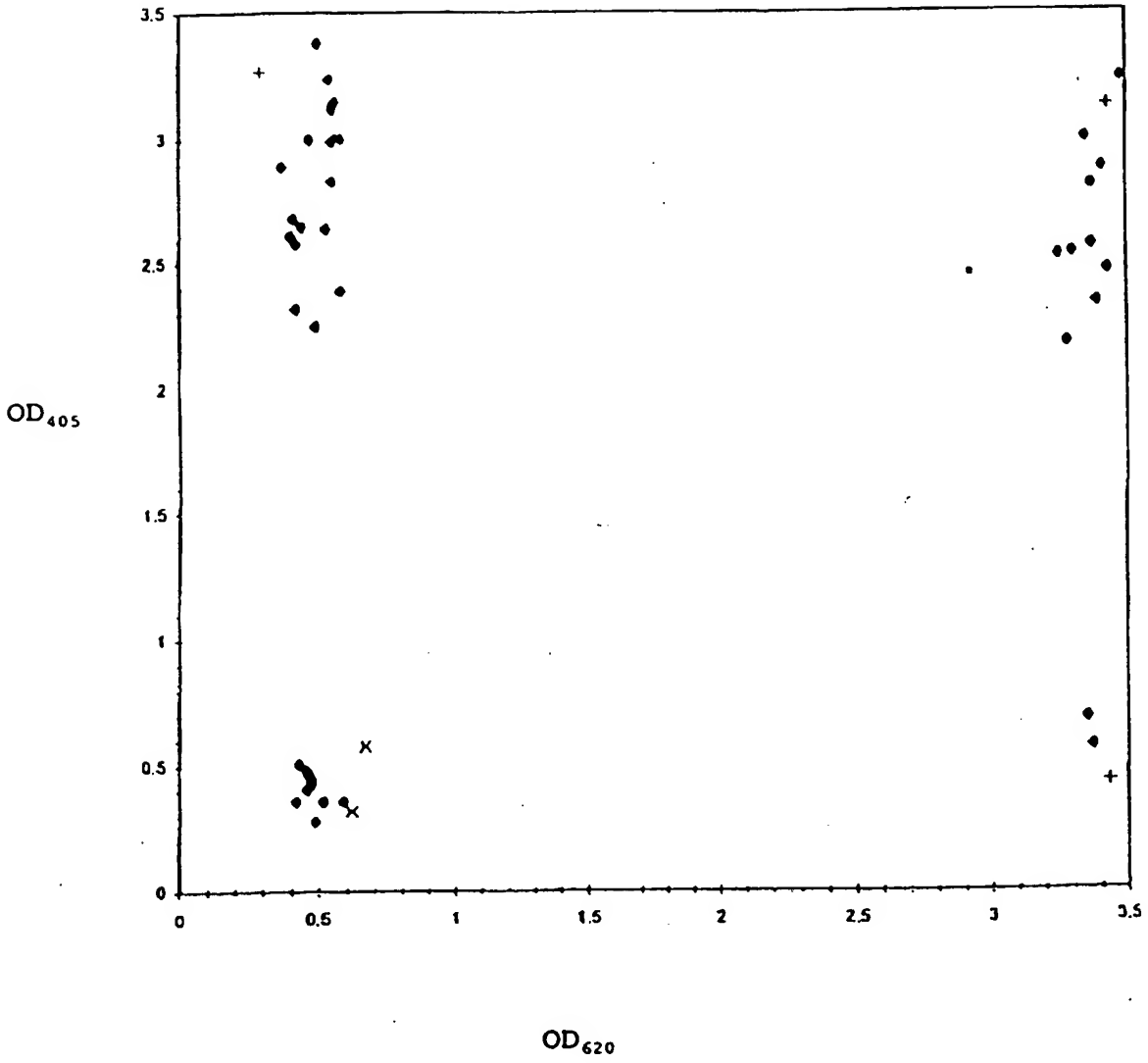


FIGURE 3